

OM protein - protein search, using sw model
Run on: January 28, 2007, 17:28:16 ; Search time 217 Seconds
(Without alignments)
1348.486 Million cell updates/sec

Title: US-10-677-669-69
Perfect score: 3135
Sequence: 1 MCSRVPLLPLLLLLALGPG.....PLMGFPGLQSLPHAKPVI 598
Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5
2782304 seqs, 48933398 residues
Total number of hits satisfying chosen parameters: 2782304
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%

Database : Listing first 1500 summaries
A_Geneseq 200701.*
1: Geneseqp1980s.*
2: Geneseqp1980s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
11: Geneseqp2007s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match Length	DB ID	Description
RESULT 1				
ID	AA06484	standard; protein; 598 AA.		
DE	Human tumour-associated protein PRO357.			
PN	WO9935170-A2.			
PD	15-JUL-1999.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3135; DB 2; Length 598;		
Best Local Similarity	100.0%;	Pred. No. 4.3e-190;		
RESULT 2				
ID	AA01322	standard; protein; 598 AA.		
DE	Human PRO357 polypeptide.			
PN	WO200032776-A2.			
PD	08-JUN-2000.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3135; DB 3; Length 598;		
Best Local Similarity	100.0%;	Pred. No. 4.3e-190;		
RESULT 3				
ID	AA03691	standard; protein; 598 AA.		
DE	Amino acid sequence of novel polypeptide PRO357.			
PN	WO200037640-A2.			
PD	29-JUN-2000.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3135; DB 3; Length 598;		
Best Local Similarity	100.0%;	Pred. No. 4.3e-190;		
RESULT 4				
ID	AA03643	standard; protein; 598 AA.		
DE	Human PRO protein, Seq ID No 104.			
PN	WO200208288-A2.			
PD	31-JAN-2002.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3135; DB 5; Length 598;		
Best Local Similarity	100.0%;	Pred. No. 4.3e-190;		
RESULT 5				
ID	AD031844	standard; protein; 598 AA.		
DE	Novel human secreted and transmembrane protein PRO357.			
PN	WO200193983-A1.			
PD	13-DEC-2001.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3135; DB 5; Length 598;		
Best Local Similarity	100.0%;	Pred. No. 4.3e-190;		
RESULT 6				
ID	ABU55931	standard; protein; 598 AA.		

DE Human secreted/transmembrane protein PRO357.
PN US2002142959-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 7
ID ABU0790 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 8
ID ABO33756 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003045687-A1.
PD 05-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 9
ID ABU60241 standard; protein; 598 AA.
DE Human PRO polypeptide #12.
PN US2002132768-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 10
ID ABU64927 standard; protein; 598 AA.
DE Human secreted/transmembrane protein PRO357.
PN US2002173463-A1.
PD 21-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 11
ID ABU58361 standard; protein; 598 AA.
DE Novel human secreted protein PRO357.
PN US2002150976-A1.
PD 17-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 12
ID ABU57247 standard; protein; 598 AA.
DE Human PRO357 protein.
PN US2002142958-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 13
ID ABU56312 standard; protein; 598 AA.
DE Human secreted/transmembrane protein, PRO357.
PN US2002132981-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 14
ID ABU60352 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2002168715-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 15
ID ABU82099 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.

PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 16
ID ABU11313 standard; protein; 598 AA.
DE Human PRO357 protein sequence.
PN US2002127643-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 17
ID ABU67132 standard; protein; 598 AA.
DE Human PRO polypeptide #12.
PN US2002165143-A1.
PD 07-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 18
ID ASJ72279 standard; protein; 598 AA.
DE Human PRO357 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 19
ID ASJ72407 standard; protein; 598 AA.
DE Human PRO357 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 20
ID ASO34302 standard; protein; 598 AA.
DE Human secreted/transmembrane polypeptide PRO 357.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 21
ID ASJ72109 standard; protein; 598 AA.
DE Human membrane bound receptor/protein PRO357 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 22
ID ADB83594 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 23
ID ADB80700 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 24
ID ADB73241 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096968-A1.

PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 25
ID ADB78323 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 26
ID ADB84971 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 27
ID ADB78077 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 28
ID ADB87143 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 29
ID ADB84725 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 30
ID ADB83840 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 31
ID ADB72995 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 32
ID ADC25825 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2002142419-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 33
ID ADC25583 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2002156004-A1.
PD 24-OCT-2002.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 34
ID ADC25704 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2003077698-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 35
ID ADC36833 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 36
ID ADC21823 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 37
ID ADC49854 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 38
ID ADC49053 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 39
ID ADC49570 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 40
ID ADC47431 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 41
ID ADC47176 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 42
ID ADC78051 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 43
ID ADD06286 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 44
ID ADC77805 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 45
ID ADD50768 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 46
ID ADD51014 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 47
ID ADD50495 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 48
ID ADD50249 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 49
ID ADD51260 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 50
ID ADH27489 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2003083479-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 51
ID ADC48807 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;

Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 52
ID ADE20978 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 53
ID ADE05822 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 54
ID ADE75051 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 55
ID ADE75797 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 56
ID ADE85029 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 57
ID ADE86855 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 58
ID ADE20732 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 59
ID ADE39029 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 60
ID ADE05576 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 61
ID ADD73561 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 62
ID ADD78401 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 63
ID ADE21224 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 64
ID ADD77339 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 65
ID ADE20486 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 66
ID ADD75551 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 67
ID ADD74067 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 68
ID ADD74313 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 69
ID ADD76043 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 70

ID ADD85535 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 71
ID ADE05084 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 72
ID ADD75297 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 73
ID ADD76841 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 74
ID ADD86609 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 75
ID ADD78077 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 76
ID ADE71538 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2003096742-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 77
ID ADD77585 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 78
ID ADD77831 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 79
ID ADD85289 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 80
ID ADD73821 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 81
ID ADD74559 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 82
ID ADD77087 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 83
ID ADD85781 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 84
ID ADE05330 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 85
ID ADD74805 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 86
ID ADE05617 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 87
ID ADG27171 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 88
ID ADG11234 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.

PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 89
ID ADG12013 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 90
ID ADF94570 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 91
ID ADG06666 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 92
ID ADG63481 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2003211570-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 93
ID ADH39010 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 94
ID ADH43210 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2003207401-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 95
ID ADG34100 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 96
ID ADI33570 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 97
ID ADH69664 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2004019183-A1.

PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 98
ID ADI29825 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 99
ID ADM27222 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 100
ID ADK66580 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 101
ID ADN00448 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2004091972-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 102
ID ADU25372 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2004220385-A1.
PD 04-NOV-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 103
ID ADY39535 standard; protein; 598 AA.
DE Human insulin-like growth factor homolog PRO357 precursor protein.
PN US2005048613-A1.
PD 03-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 9; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 104
ID ADY73816 standard; protein; 598 AA.
DE Human PRO357 protein, SEQ ID NO: 69.
PN US2005059115-A1.
PD 17-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 9; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 105
ID AEG19662 standard; protein; 598 AA.
DE Human secreted protein PRO357.
PN W02006026222-A2.
PD 09-MAR-2006.
PA (GETH) GENENTECH INC.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 100.0%; Score 3135; DB 10; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 106
ID AHS0165 standard; protein; 598 AA.
DE Human cDNA clone DNA44804-1248 protein product PRO357 SEQ ID NO: 69.
PN US2006105427-A1.

PA 18-MAY-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 10; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 107
ID AEU49290 standard; protein; 598 AA.
DE Human secreted polypeptide PRO357, SEQ ID NO:104.
PN EPI659177-A2.
PD 24-MAY-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 10; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 108
ID AEI36373 standard; protein; 598 AA.
DE Human PRO protein amino acid sequence - SEQ ID 69.
PN US2006127983-A1.
PD 15-JUN-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 10; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 109
ID AEK48325 standard; protein; 598 AA.
DE Human PRO357 amino acid sequence.
PN EPI686174-A1.
PD 02-AUG-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 10; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 110
ID AEK62918 standard; protein; 598 AA.
DE Human PRO357 polypeptide, SEQ ID NO: 104.
PN EPI700867-A2.
PD 13-SEP-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 10; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 111
ID AEI6958 standard; protein; 598 AA.
DE Human secreted polypeptide PRO357, SEQ ID NO:104.
PN EPI702928-A2.
PD 20-SEP-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 10; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 112
ID AAY17831 standard; protein; 598 AA.
DE Human PRO357 protein sequence.
PN WQ928462-A2.
PD 10-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 99.7%; Score 3126; DB 2; Length 598;
Best Local Similarity 99.8%; Pred. No. 1.6e-189;
RESULT 113
ID AAB07428 standard; protein; 673 AA.
DE Amino acid sequence of a leucine-rich surface glycoprotein (LRSG).
PN W0200042170-A1.
PD 20-JUL-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 98.4%; Score 3083.5; DB 3; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 114
ID AAB87533 standard; protein; 673 AA.
DE Human PRO1282.
PN W0200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 4; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 115
ID AAB65166 standard; protein; 673 AA.
DE Human PRO1282 (UNQ652) protein sequence SEQ ID NO:52.
PN W0200073454-A1.
PD 07-DEC-2000.

PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 4; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 116
ID AAU75266 standard; protein; 673 AA.
DE Human Slit-like protein #1.
PN W0200212346-A2.
PD 14-FEB-2002.
PA (PHAA) PHARMACIA CORP.
Query Match 98.4%; Score 3083.5; DB 5; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 117
ID ARG95858 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 5; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 118
ID AEG78042 standard; protein; 673 AA.
DE Human leucine-rich surface glycoprotein (LRSG-1).
PN US2002072089-A1.
PD 13-JUN-2002.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (MACB/) MACBETH K J.
PA (BUSF/) BUSFIELD S J.
PA (PANT/) PAN Y.
PA (WHIT/) WHITE D.
PA (KHOD/) KHODADOUST M M.
PA (GUNW/) GU W.
Query Match 98.4%; Score 3083.5; DB 5; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 119
ID ABU57981 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 120
ID ABU59059 standard; protein; 673 AA.
DE Novel human secreted or transmembrane protein PRO1282.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 121
ID ABU82571 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 122
ID ABU60490 standard; protein; 673 AA.
DE Human secreted/transmembrane protein, #19.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 123
ID ABU13872 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 124

ID ABU72457 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 125
ID ABU90883 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 126
ID ABO33942 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 127
ID ABU71959 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 128
ID ABU71513 standard; protein; 673 AA.
DE Human secreted polypeptide PRO1282.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 129
ID ABU72294 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 130
ID ABU90967 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 131
ID ABU59206 standard; protein; 673 AA.
DE Human secreted/transmembrane protein, #19.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 132
ID ABO25903 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 133
ID ABO27288 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO1282.

PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 134
ID ABU92483 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 135
ID ABU81153 standard; protein; 673 AA.
DE Human secreted polypeptide PRO1282.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 136
ID ABO53268 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 137
ID ABU58912 standard; protein; 673 AA.
DE Human secreted/transmembrane protein, #19.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 138
ID ABU92290 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 139
ID ABU59355 standard; protein; 673 AA.
DE Novel human secreted or transmembrane protein PRO1282.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 140
ID ABU98270 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 141
ID ABU89275 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 142
ID ABU82482 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.

Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 143
ID ABU92121 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 144
ID ABU96446 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 145
ID ABU10827 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 146
ID ABU81579 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 147
ID ABU72116 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 148
ID ABU88518 standard; protein; 673 AA.
DE Human secreted and transmembrane polypeptide PRO1282.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 149
ID ABO34032 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 150
ID ABO17073 standard; protein; 673 AA.
DE Human transmembrane PRO polypeptide (SeqID 16).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 151
ID ADA37563 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 152

ID ADA21249 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO1282.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 153
ID ABO44246 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO 1282.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 154
ID ADA10036 standard; protein; 673 AA.
DE Human secreted/transmembrane protein, PRO1282.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 155
ID ADA19878 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US200306394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 156
ID AOB17261 standard; protein; 673 AA.
DE Human transmembrane PRO polypeptide (SeqID 16).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 157
ID ADA17580 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 158
ID ADA27688 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 159
ID ADA20050 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 160
ID ABO34174 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO 1282.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 161
ID ADA94268 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;

Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 162
ID ADA38493 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
FN US2003059780-A1.
PD 27-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 163
ID ADA92614 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
FN US2003060407-A1.
PD 27-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 164
ID ADA00347 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO 1282.
FN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 165
ID ABO53118 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
FN US2003044806-A1.
PD 06-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 166
ID ADA22175 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO1282.
FN US2003040473-A1.
PD 27-FEB-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 167
ID ABO22488 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
FN US2003017982-A1.
PD 23-JAN-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 168
ID ADA06341 standard; protein; 673 AA.
DE Human secreted/transmembrane PRO polypeptide #13.
FN US2003049638-A1.
PD 13-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 169
ID ADA39034 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
FN US2003059782-A1.
PD 27-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 170
ID ADB85589 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
FN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 171
ID AD96060 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
FN US2003054403-A1.
PD 20-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 172
ID ADB68268 standard; protein; 673 AA.
DE Human PRO1282 protein.
FN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 173
ID ADB68075 standard; protein; 673 AA.
DE Human PRO1282 protein.
FN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 174
ID ADB90892 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
FN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 175
ID ADC57532 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
FN US2003027754-A1.
PD 06-FEB-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 176
ID ADC54896 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
FN US2003045463-A1.
PD 06-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 177
ID ADC11763 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
FN US2003049681-A1.
PD 13-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 178
ID ADC06972 standard; protein; 673 AA.
DE Human PRO1282 protein.
FN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 179
ID ADC56185 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
FN US2003064375-A1.
PD 03-APR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 180
ID ADC17151 standard; protein; 673 AA.
DE Mammalian PRO polypeptide (SeqID 16).
FN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 181
ID ADC07240 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
FN US2003068647-A1.
PD 10-APR-2003.

Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 182
ID ADC11230 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 183
ID ADC14849 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 184
ID ADC52344 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 185
ID ADC14352 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 186
ID ADD07884 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003086623-A1.
PD 10-APR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 187
ID ADC81709 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 188
ID ADD07351 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 189
ID ADC82242 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 190
ID ADD08422 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 191
ID ADD06671 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2002193300-A1.
PD 19-DEC-2002.

PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 192
ID ADC82918 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 193
ID ADD55025 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 194
ID ADD36020 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 195
ID ADD55983 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 196
ID ADD54421 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 197
ID ADE26575 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 198
ID ADE26042 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 199
ID ADF66979 standard; protein; 673 AA.
DE Human PRO1282 amino acid sequence SEQ ID NO:52.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 200
ID ADG01021 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 201
ID ADG08574 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.

PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 202
ID ADF95195 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 203
ID ADH24048 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 204
ID ADH34074 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 205
ID ADH29907 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 206
ID ADH23878 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 207
ID ADG85282 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 208
ID ADH24558 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 209
ID ADH37414 standard; protein; 673 AA.
DE Human secreted and transmembrane protein PRO1282.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 210
ID ADH02003 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003180837-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 211
ID ADH37584 standard; protein; 673 AA.
DE Human secreted and transmembrane protein PRO1282.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 212
ID ADG85622 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 213
ID ADH24218 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 214
ID ADH38512 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 215
ID ADG83633 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 216
ID ADH29441 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 217
ID ADH27557 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 218
ID ADH37754 standard; protein; 673 AA.
DE Human secreted and transmembrane protein PRO1282.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 219
ID ADH37931 standard; protein; 673 AA.
DE Human secreted and transmembrane protein PRO1282.
PN US2003181649-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 220
ID ADH57351 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 221
ID ADH53493 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 222
ID ADH53663 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 223
ID ADH51999 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 224
ID ADH49854 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 225
ID ADI25364 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 226
ID ADH90157 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 227
ID ADI25534 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 228
ID ADH97708 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 229
ID ADI35233 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 230
ID ADI03556 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 231
ID ADI11913 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 232
ID ADH89987 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 233
ID ADH9725 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 234
ID ADH98388 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 235
ID ADI11063 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 236
ID ADI11573 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 237
ID ADH98218 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 238
ID ADH97708 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

ID ADH98558 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 239
ID ADH98048 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 240
ID ADI05036 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 241
ID ADI03386 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 242
ID ADI04781 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 243
ID ADH78235 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 244
ID ADI19579 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 245
ID ADH90327 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 246
ID ADI03046 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
ID ADH77895 standard; protein; 673 AA.

DE Human PRO polypeptide #8.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 248
ID ADH97878 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 249
ID ADI01263 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 250
ID ADI01958 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 251
ID ADI03216 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 252
ID ADI11403 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 253
ID ADI02305 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 254
ID ADI11743 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 255
ID ADI05380 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
ID ADH79452 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.

PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 257
ID ADI19409 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 258
ID ADI05210 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 259
ID ADH79622 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 260
ID ADI01448 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 261
ID ADI01618 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 262
ID ADI01788 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 263
ID ADH79792 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 264
ID ADI04610 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 265
ID ADI02746 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181651-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 266
ID ADH78065 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 267
ID ADI25704 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 268
ID ADI25874 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 269
ID ADK65386 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 270
ID ADH98728 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 271
ID ADH79969 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 272
ID ADL93700 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 273
ID ADC52154 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 274
ID ADF35178 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.

Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 275
ID ADG11428 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 276
ID ADH06586 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 277
ID ADH06416 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 278
ID ADG68837 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 279
ID ADH27727 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 280
ID ADH25068 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 281
ID ADH33700 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 282
ID ADH02343 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 283
ID ADH07950 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;

Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 284
ID ADG69347 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 285
ID ADH39168 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 286
ID ADG83908 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 287
ID ADH19298 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 288
ID ADG85452 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 289
ID ADH06246 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 290
ID ADH30076 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 291
ID ADH24388 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 292
ID ADG69517 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;

RESULT 293
ID ADH07780 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 8; Length 673;
Pred. No. 9.1e-187;
RESULT 294
ID ADG85792 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 8; Length 673;
Pred. No. 9.1e-187;
RESULT 295
ID ADH39338 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 8; Length 673;
Pred. No. 9.1e-187;
RESULT 296
ID ADH33530 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 8; Length 673;
Pred. No. 9.1e-187;
RESULT 297
ID ADH33870 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 8; Length 673;
Pred. No. 9.1e-187;
RESULT 298
ID ADH01080 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 8; Length 673;
Pred. No. 9.1e-187;
RESULT 299
ID ADG69687 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 8; Length 673;
Pred. No. 9.1e-187;
RESULT 300
ID ADH20791 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 8; Length 673;
Pred. No. 9.1e-187;
RESULT 301
ID ADH02173 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 8; Length 673;
Pred. No. 9.1e-187;
RESULT 302
ID ADG69177 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 8; Length 673;
Pred. No. 9.1e-187;
RESULT 303
ID ADG85962 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 8; Length 673;
Pred. No. 9.1e-187;
RESULT 304
ID ADH24898 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 8; Length 673;
Pred. No. 9.1e-187;
RESULT 305
ID ADH39515 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 8; Length 673;
Pred. No. 9.1e-187;
RESULT 306
ID ADH19831 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 8; Length 673;
Pred. No. 9.1e-187;
RESULT 307
ID ADH02513 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 8; Length 673;
Pred. No. 9.1e-187;
RESULT 308
ID ADG69007 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 8; Length 673;
Pred. No. 9.1e-187;
RESULT 309
ID ADH07610 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 8; Length 673;
Pred. No. 9.1e-187;
RESULT 310
ID ADG86132 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 8; Length 673;
Pred. No. 9.1e-187;
RESULT 311
ID ADH24728 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 8; Length 673;
Pred. No. 9.1e-187;

PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 312
ID ADH25776 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 313
ID ADH38342 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 314
ID ADH57181 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 315
ID ADH52169 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 316
ID ADH49535 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 317
ID ADH90497 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 318
ID ADI11233 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 319
ID ADH9898 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 320
ID ADI02128 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003190699-A1.

PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 321
ID ADH90667 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 322
ID ADJ98542 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181797-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 323
ID ADJ98712 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 324
ID ADH78871 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 325
ID ADJ99105 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 326
ID ADJ99275 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 327
ID ADJ98893 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 328
ID ADH79041 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 329
ID ADK00901 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003186407-A1.
PD 02-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 330
ID ADK14422 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 331
ID ADM80871 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 332
ID ADR45587 standard; protein; 673 AA.
DE Human leucine-rich surface glycoprotein, LRSG-1, protein #1.
PN US2004176296-A1.
PD 09-SEP-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 333
ID ADY77711 standard; protein; 673 AA.
DE Neoplastic disease detection protein PRO1282.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO)/ EATON D L.
PA (FILV)/ FILVAROFF E.
PA (GERR)/ GERRITSEN M E.
PA (GODD)/ GODDARD A.
PA (GODO)/ GODOWSKI P J.
PA (GRIM)/ GRIMALDI J C.
PA (GURN)/ GURNEY A L.
PA (WATA)/ WATANABE C K.
PA (WOOD)/ WOOD W I.
Query Match 98.4%; Score 3083.5; DB 9; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 334
ID ABA38367 standard; protein; 673 AA.
DE Human secreted/transmembrane protein, #81.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 9; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 335
ID AEF12542 standard; protein; 673 AA.
DE Human PRO1282 protein SEQ ID NO:16.
PN US2006008901-A1.
PD 12-JAN-2006.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 10; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 336
ID AEF74231 standard; protein; 673 AA.
DE Human PRO1282 protein SEQ ID NO:16.
PN US2005260647-A1.
PD 24-NOV-2005.
PA (EATO)/ EATON D L.
PA (FILV)/ FILVAROFF E.
PA (GERR)/ GERRITSEN M E.
PA (GODD)/ GODDARD A.
PA (GODO)/ GODOWSKI P J.
PA (GRIM)/ GRIMALDI J C.
PA (GURN)/ GURNEY A L.
PA (WATA)/ WATANABE C K.
PA (WOOD)/ WOOD W L.

Query Match 98.4%; Score 3083.5; DB 10; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 337
ID AEH43569 standard; protein; 673 AA.
DE PRO1282 protein sequence, SEQ ID 16.
PN US2006099657-A1.
PD 11-MAY-2006.
PA (EATO)/ EATON D L.
PA (FILV)/ FILVAROFF E.
PA (GERR)/ GERRITSEN M E.
PA (GODD)/ GODDARD A.
PA (GODO)/ GODOWSKI P J.
PA (GRIM)/ GRIMALDI J C.
PA (GURN)/ GURNEY A L.
PA (WATA)/ WATANABE C K.
PA (WOOD)/ WOOD W I.
Query Match 98.4%; Score 3083.5; DB 10; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 338
ID ASJ11894 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2006160186-A1.
PD 20-JUL-2006.
PA (EATO)/ EATON D L.
PA (FILV)/ FILVAROFF E.
PA (GERR)/ GERRITSEN M E.
PA (GODD)/ GODDARD A.
PA (GODO)/ GODOWSKI P J.
PA (GRIM)/ GRIMALDI J C.
PA (GURN)/ GURNEY A L.
PA (WATA)/ WATANABE C K.
PA (WOOD)/ WOOD W I.
Query Match 98.4%; Score 3083.5; DB 10; Length 673;
Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 339
ID AAB84689 standard; protein; 673 AA.
DE Amino acid sequence of human slit polypeptide Zslit3.
PN WO200146418-A1.
PD 28-JUN-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 98.2%; Score 3078.5; DB 4; Length 673;
Best Local Similarity 88.6%; Pred. No. 1.9e-186;
RESULT 340
ID ADF69108 standard; protein; 673 AA.
DE Human MP53 protein sequence SEQ ID NO:78.
PN WO2003083047-A2.
PD 09-OCT-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 98.2%; Score 3078.5; DB 7; Length 673;
Best Local Similarity 88.6%; Pred. No. 1.9e-186;
RESULT 341
ID AEL57287 standard; protein; 673 AA.
DE Human glomerulus-specific marker, SEQ ID NO: 1750.
PN US2006216722-A1.
PD 28-SEP-2006.
PA (BETS)/ BETSHOLTZ C.
PA (TRYG)/ TRYGGVASON K.
PA (TAKE)/ TAKEMOTO M.
PA (HELL/) HE L.
PA (PATR)/ PATRAKKAS J.
Query Match 98.2%; Score 3078.5; DB 10; Length 673;
Best Local Similarity 88.6%; Pred. No. 1.9e-186;
RESULT 342
ID AEO59449 standard; protein; 676 AA.
DE Human genome derived single exon protein #5683.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN)/ PENN S G.
PA (RANK)/ RANK D R.
PA (HANZ)/ HANZEL D K.
Query Match 98.2%; Score 3078.5; DB 8; Length 676;
Best Local Similarity 88.6%; Pred. No. 1.9e-186;
RESULT 343

ID ADA57213 standard; protein; 672 AA.
DE Human secreted protein #496.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 93.6%; Score 2935; DB 6; Length 672;
Best Local Similarity 85.2%; Pred. No. 2.3e-177;
RESULT 344
ID ADA41092 standard; protein; 672 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 93.6%; Score 2935; DB 6; Length 672;
Best Local Similarity 85.2%; Pred. No. 2.3e-177;
RESULT 345
ID ABR47923 standard; protein; 672 AA.
DE Human secreted protein, SEQ ID 814.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 93.6%; Score 2935; DB 6; Length 672;
Best Local Similarity 85.2%; Pred. No. 2.3e-177;
RESULT 346
ID AEL29423 standard; protein; 672 AA.
DE Human secreted protein, SEQ ID 1403.
PN US2006223088-A1.
PD 05-OCT-2006.
Query Match 93.6%; Score 2935; DB 10; Length 672;
Best Local Similarity 85.2%; Pred. No. 2.3e-177;
RESULT 347
ID AEL94636 standard; protein; 672 AA.
DE Human secreted protein amino acid sequence - SEQ ID 817.
PN US2006246483-A1.
PD 02-NOV-2006.
Query Match 93.6%; Score 2935; DB 10; Length 672;
Best Local Similarity 85.2%; Pred. No. 2.3e-177;
RESULT 348
ID AAB38323 standard; protein; 673 AA.
DE Human secreted protein encoded by gene 3 clone HSYAV50.
PN WO2000061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 93.6%; Score 2935; DB 3; Length 673;
Best Local Similarity 85.2%; Pred. No. 2.3e-177;
RESULT 349
ID AAB38400 standard; peptide; 723 AA.
DE Fragment of human secreted protein encoded by gene 3 clone HSYAV50.
PN WO2000061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 93.6%; Score 2935; DB 3; Length 673;
Best Local Similarity 85.2%; Pred. No. 2.5e-177;
RESULT 350
ID AAU75267 standard; protein; 630 AA.
DE Human slit-like protein #2.
PN WO200212346-A2.
PD 14-FEB-2002.
PA (PHAA-) PHARMACIA CORP.
Query Match 90.8%; Score 2845.5; DB 5; Length 630;
Best Local Similarity 85.2%; Pred. No. 1e-171;
RESULT 351
ID AA166643 standard; protein; 611 AA.
DE Membrane-bound protein PRO1282.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH-) GENENTECH INC.
Query Match 86.5%; Score 2712.5; DB 3; Length 611;
Best Local Similarity 79.5%; Pred. No. 2.6e-163;
RESULT 352
ID ABG78046 standard; protein; 673 AA.
DE Mouse leucine-rich surface glycoprotein (LRSG-1).
PN US2002072089-A1.

PD 13-JUN-2002.
PA (HOLT-) HOLTZMAN D A.
PA (MCCA-) MCCARTHY S A.
PA (MACB-) MACHETH K J.
PA (BUSF-) BUSFIELD S J.
PA (PANY-) PAN Y.
PA (WHIT-) WHITE D.
PA (KHOD-) KHODADOUST M M.
PA (GUWW-) GU W.
Query Match 79.4%; Score 2490; DB 5; Length 673;
Best Local Similarity 73.5%; Pred. No. 3.6e-149;
RESULT 353
ID ADR45596 standard; protein; 673 AA.
DE Human leucine-rich surface glycoprotein, LRSG-1, protein #2.
PN US2004176296-A1.
PD 09-SEP-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 79.4%; Score 2490; DB 8; Length 673;
Best Local Similarity 73.5%; Pred. No. 3.6e-149;
RESULT 354
ID AEL56067 standard; protein; 673 AA.
DE Mouse slit-like 2, SEQ ID NO: 526.
PN US2006216722-A1.
PD 28-SEP-2006.
PA (BETS-) BETSHOLTZ C.
PA (TRYG-) TRYGVASON K.
PA (TAKE-) TAKEMOTO M.
PA (HELL-) HE L.
PA (PATR-) PATRAKKAS J.
Query Match 79.4%; Score 2490; DB 10; Length 673;
Best Local Similarity 73.5%; Pred. No. 3.6e-149;
RESULT 355
ID ADA00753 standard; protein; 673 AA.
DE Murine stromal cell derived haematopoietin factor-5 SEQ ID NO:10.
PN WO2003018805-A1.
PD 06-MAR-2003.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA (NINA-) JAPAN NAT CANCER CENT.
Query Match 79.2%; Score 2484; DB 6; Length 673;
Best Local Similarity 73.4%; Pred. No. 8.7e-149;
RESULT 356
ID AAB07431 standard; protein; 493 AA.
DE A leucine-rich surface glycoprotein (LRSG).
PN WO200042170-A1.
PD 20-JUL-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 53.3%; Score 1672; DB 3; Length 493;
Best Local Similarity 53.3%; Pred. No. 1.7e-97;
RESULT 357
ID ABB72324 standard; protein; 281 AA.
DE Rat protein isolated from skin cells SEQ ID NO: 648.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 37.6%; Score 1178.5; DB 5; Length 281;
Best Local Similarity 80.7%; Pred. No. 1.6e-66;
RESULT 358
ID AAO30403 standard; protein; 311 AA.
DE Human secreted protein (SECP)-6.
PN WO2003046196-A1.
PD 05-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 31.8%; Score 997.5; DB 7; Length 311;
Best Local Similarity 68.7%; Pred. No. 5.3e-55;
RESULT 359
ID ABR58506 standard; protein; 307 AA.
DE Human secreted protein Incyte ID No: 7500228CD1 SEQ ID NO: 18.
PN WO2003029437-A2.
PD 10-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 31.3%; Score 980.5; DB 6; Length 307;
Best Local Similarity 67.9%; Pred. No. 6.2e-54;
RESULT 360

ID AAO30821 standard; protein; 117 AA.
DE Human cell adhesion and extracellular matrix protein (CADECM)-11.
PN WO2003047526-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 15.0%; Score 471; DB 7; Length 117;
Best Local Similarity 98.9%; Pred. No. 3.8e-22;
RESULT 361
ID AAE23980 standard; protein; 635 AA.
DE Human LP220 secreted protein.
PN WO200226801-A2.
PD 04-APR-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 11.5%; Score 360.5; DB 5; Length 635;
Best Local Similarity 27.1%; Pred. No. 2.7e-14;
RESULT 362
ID ABP70142 standard; protein; 647 AA.
DE Human NOV44a.
PN WO200272771-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 11.5%; Score 360.5; DB 5; Length 647;
Best Local Similarity 27.1%; Pred. No. 2.8e-14;
RESULT 363
ID AAO26256 standard; protein; 635 AA.
DE MDDT related human protein SEQ ID No 34.
PN WO200296951-A1.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.5%; Score 359.5; DB 6; Length 635;
Best Local Similarity 27.8%; Pred. No. 3.2e-14;
RESULT 364
ID AD209859 standard; protein; 635 AA.
DE Human breast cancer marker MGC3103 protein.
PN EP1522594-A2.
PD 13-APR-2005.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 11.5%; Score 359.5; DB 9; Length 635;
Best Local Similarity 27.6%; Pred. No. 3.2e-14;
RESULT 365
ID ABP70144 standard; protein; 778 AA.
DE Human NOV44c.
PN WO200272771-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 11.4%; Score 357.5; DB 5; Length 778;
Best Local Similarity 26.7%; Pred. No. 5.4e-14;
RESULT 366
ID ADM90979 standard; protein; 545 AA.
DE Human pharmaceutically useful protein seqID 372.
PN WO2004020595-A2.
PD 11-MAR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.
PA (DNAP-) DNAPFORM KK.
Query Match 11.2%; Score 350.5; DB 8; Length 545;
Best Local Similarity 27.9%; Pred. No. 9.9e-14;
RESULT 367
ID ABP70143 standard; protein; 566 AA.
DE Human NOV44b.
PN WO200272771-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 10.8%; Score 339; DB 5; Length 566;
Best Local Similarity 26.9%; Pred. No. 5.5e-13;
RESULT 368
ID AAE17484 standard; protein; 551 AA.
DE Human leucine-rich repeat-8 (ZLRR8) protein #2.
PN WO200202604-A2.
PD 10-JAN-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 10.8%; Score 338; DB 5; Length 551;
Best Local Similarity 27.4%; Pred. No. 6.2e-13;

RESULT 369
ID ADI21104 standard; protein; 618 AA.
DE Novel human protein #79.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 10.7%; Score 337; DB 7; Length 618;
Best Local Similarity 27.2%; Pred. No. 8.2e-13;
RESULT 370
ID ADA23287 standard; protein; 653 AA.
DE Human SECX polypeptide, SECS #1.
PN US2003054514-A1.
PD 20-MAR-2003.
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
Query Match 10.7%; Score 337; DB 6; Length 653;
Best Local Similarity 23.6%; Pred. No. 8.7e-13;
RESULT 371
ID AAB23033 standard; protein; 694 AA.
DE Human SLIT protein-like splice variant, SECX 3352358-1.
PN WO200053742-A2.
PD 14-SEP-2000.
PA (CURA-) CURAGEN CORP.
Query Match 10.7%; Score 337; DB 3; Length 694;
Best Local Similarity 23.6%; Pred. No. 9.4e-13;
RESULT 372
ID AAB23034 standard; protein; 590 AA.
DE Human SLIT protein-like splice variant, SECX 3352358-2.
PN WO200053742-A2.
PD 14-SEP-2000.
PA (CURA-) CURAGEN CORP.
Query Match 10.6%; Score 333; DB 3; Length 590;
Best Local Similarity 25.8%; Pred. No. 1.4e-12;
RESULT 373
ID ADA23289 standard; protein; 590 AA.
DE Human SECX polypeptide, SEC6.
PN US2003054514-A1.
PD 20-MAR-2003.
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
Query Match 10.6%; Score 333; DB 6; Length 590;
Best Local Similarity 25.8%; Pred. No. 1.4e-12;
RESULT 374
ID ABG04827 standard; protein; 526 AA.
DE Novel human diagnostic protein #4818.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.6%; Score 332; DB 4; Length 526;
Best Local Similarity 26.9%; Pred. No. 1.4e-12;
RESULT 375
ID AAY28806 standard; protein; 653 AA.
DE cc359 4 secreted protein.
PN WO9850405-A1.
PD 07-OCT-1999.
PA (GEMY) GENETICS INST INC.
Query Match 10.5%; Score 330; DB 2; Length 653;
Best Local Similarity 24.2%; Pred. No. 2.4e-12;
RESULT 376
ID AAY66694 standard; protein; 653 AA.
DE Membrane-bound protein PRO1111.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 3; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 377
ID AAB24073 standard; protein; 653 AA.
DE Human PRO1111 protein sequence SEQ ID NO:46.
PN WO200053755-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 3; Length 653;

Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 378
ID AAU12390 standard; protein; 653 AA.
DE Human PRO1111 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 4; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 379
ID AAE09438 standard; protein; 653 AA.
DE Human sbgPRO331a protein.
PN WO200160850-A1.
PD 23-AUG-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 10.5%; Score 330; DB 4; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 380
ID AAB65217 standard; protein; 653 AA.
DE Human PRO1111 (UNQ554) protein sequence SEQ ID NO:229.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 4; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 381
ID ABUS8032 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 382
ID ABUS9110 standard; protein; 653 AA.
DE Novel human secreted or transmembrane protein PRO1111.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 383
ID ABUS2622 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 384
ID ABO17834 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 385
ID ABUS0541 standard; protein; 653 AA.
DE Human secreted/transmembrane protein, #93.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 386
ID ABUI3923 standard; protein; 653 AA.
DE Human PRO1111 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 387
ID ABUS9241 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.

ID ABUS1088 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 388
ID ABU72508 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 389
ID ABUS66788 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 390
ID AAO23105 standard; protein; 653 AA.
DE NAG14 'human modifier of p53 pathway' protein.
PN WO2003035833-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 391
ID ABUS9869 standard; protein; 653 AA.
DE Novel secreted and transmembrane protein PRO1111.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 392
ID ABUS9257 standard; protein; 653 AA.
DE Human secreted/transmembrane protein, #93.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 393
ID ABO25954 standard; protein; 653 AA.
DE Human PRO1111 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 394
ID ABO25059 standard; protein; 653 AA.
DE Human secreted/transmembrane protein (PRO) #219.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 395
ID ABUS8963 standard; protein; 653 AA.
DE Human secreted/transmembrane protein, #93.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 396
ID ABUS9241 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.

PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 397
ID ABUS9406 standard; protein; 653 AA.
DE Novel human secreted or transmembrane protein PRO1344.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 398
ID ABUS7064 standard; protein; 653 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 438.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 399
ID ABUS2172 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 400
ID ABUS10878 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 401
ID ABUS1630 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 402
ID ABUS8569 standard; protein; 653 AA.
DE Human secreted and transmembrane polypeptide PRO1111.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 403
ID ABO34083 standard; protein; 653 AA.
DE Human PRO1111 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 404
ID ADA45957 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 405
ID ADA76388 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;

RESULT 406
ID ADA19038 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 407
ID ADA61661 standard; protein; 653 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 408
ID ADB19446 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 409
ID ADB27987 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 410
ID ADA86466 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 411
ID ADB16030 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 412
ID ADA37740 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US200308297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 413
ID ADA47816 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 414
ID ADA21426 standard; protein; 653 AA.
DE Human secreted/transmembrane polypeptide PRO1111.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 415
ID ADA10213 standard; protein; 653 AA.

DE Human secreted/transmembrane protein, PRO1111.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 416
ID ADA67611 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 417
ID ADB30618 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 418
ID ADA85914 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 419
ID ADA17757 standard; protein; 653 AA.
DE Human PRO1111 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 420
ID ADA97126 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 421
ID ADA79430 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 422
ID ADA87569 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 423
ID ADB16771 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 424
ID ADA27865 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003054359-A1.
PD 20-MAR-2003.

Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 425
ID ADA91963 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 426
ID ADB14926 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 427
ID ADB18887 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 428
ID ADA94102 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 429
ID ADB19998 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 430
ID ADB13310 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 431
ID ABO43367 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 432
ID ADA94445 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 433
ID ADA74564 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;

RESULT 434
ID ADB24797 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US200307713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 435
ID ADA82321 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 436
ID ADA75284 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 437
ID ADA83362 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 438
ID ADA84810 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 439
ID ADB30066 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 440
ID ADA80594 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 441
ID ADA75836 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 442
ID ADA38670 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 443
ID ADA47061 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082702-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 444
ID ADB23557 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US200307715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 445
ID ADA93533 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US200307721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 446
ID ADB26883 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 447
ID ADB31170 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 448
ID ADA92791 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 449
ID ADA61098 standard; protein; 653 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 450
ID ADB24245 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US200307714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 451
ID ADA96574 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 452
ID ADA81146 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082702-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 453
ID ADA96022 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 454
ID ADB26331 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 455
ID ADB21816 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 456
ID ADA77595 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 457
ID ADB18335 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 458
ID ADA87018 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 459
ID ADA88121 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 460
ID ADA46509 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 461
ID ADB28539 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 462
ID ADB229091 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 463
ID ABO53169 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 464
ID ADA77043 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 465
ID ADA22352 standard; protein; 653 AA.
DE Human secreted/transmembrane polypeptide PRO1111.
PN US2003040473-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 466
ID ADA88673 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 467
ID ADA97678 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 468
ID ADB27435 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 469
ID ADB22368 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 470
ID ABO22539 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003017982-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 471
ID ADA06518 standard; protein; 653 AA.
DE Human secreted/transmembrane PRO polypeptide #64.

PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 472
ID ADA39211 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 473
ID ADA67059 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 474
ID ADB22920 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 475
ID ADB23693 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 476
ID ADA92415 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 477
ID ADB15478 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 478
ID ADB38730 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 479
ID ADB96237 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 480
ID ADB38178 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 481
ID ADB66650 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 482
ID ADB89730 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 483
ID ADB90462 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 484
ID ADB39563 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 485
ID ADB47186 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 486
ID ADB86793 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 487
ID ADB77398 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 488
ID ADB34555 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 489
ID ADB35659 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;

RESULT 490
ID ADB34003 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 491
ID ADB35107 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 492
ID ADB36211 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 493
ID ADB46606 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 494
ID ADC57709 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 495
ID ADC55073 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003049681-A1.
PD 06-MAR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 496
ID ADC11940 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 497
ID ADC56362 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 498
ID ADC07417 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 499
ID ADC11407 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 500
ID ADC50479 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 501
ID ADC72026 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 502
ID ADC60005 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 503
ID ADC53012 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 504
ID ADC57366 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 505
ID ADC60557 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 506
ID ADC51032 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 507
ID ADC65559 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 508
ID ADC54657 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;

RESULT 509
ID ADC53618 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 510
ID ADC59141 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 511
ID ADC56019 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 512
ID ADC58989 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 513
ID ADC14529 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 514
ID ADD08061 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 515
ID ADD03263 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 516
ID ADC90255 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 517
ID ADC81886 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 518
ID ADC69674 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194770-A1.

PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 519
ID ADC48563 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 520
ID ADD10092 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 521
ID ADD07528 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 522
ID ADD04667 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 523
ID ADC82419 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 524
ID ADC80623 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 525
ID ADD11130 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 526
ID ADC48011 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 527
ID ADD08599 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;

Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 528
ID ADC80071 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 529
ID ADD06848 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 530
ID ADD09540 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 531
ID ADC83095 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 532
ID ADD41253 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 533
ID ADD52392 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 534
ID ADD53132 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 535
ID ADD53684 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 536
ID ADD55202 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003077593-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 537
ID ADD56160 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087304-A1.

DE Human PRO polypeptide #64.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 538
ID ADD51840 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 539
ID ADD02639 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 540
ID ADD02073 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 541
ID ADD54255 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 542
ID ADD54598 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 543
ID ADD92572 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 544
ID ADD91468 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 545
ID ADE04082 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 546
ID ADE26752 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087304-A1.

PD 08-MAY-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 547
ID ADE33379 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 548
ID ADE22311 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 549
ID ADD79535 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 550
ID ADE42071 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 551
ID ADE17888 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 552
ID ADD92020 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 553
ID ADE33483 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 554
ID ADE34035 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 555
ID ADD80087 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 556
ID ADD93124 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 557
ID ADE19544 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 558
ID ADE18992 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 559
ID ADE43188 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 560
ID ADD95977 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 561
ID ADE22863 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 562
ID ADD78981 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 563
ID ADE26219 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 564
ID ADE32931 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;

RESULT 565
ID ADE42623 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 566
ID ADD80639 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 567
ID ADD89667 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 568
ID ADE40951 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 569
ID ADE04750 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 570
ID ADE92879 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 571
ID ADE67156 standard; protein; 653 AA.
DE Human PRO1111 amino acid sequence SEQ ID NO:229.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 572
ID ADG21588 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 573
ID ADG23229 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 574
ID ADE97564 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 575
ID ADG80628 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 576
ID ADG80076 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 577
ID ADH53368 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 578
ID ADH55920 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 579
ID ADI35410 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 580
ID ADI64139 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 581
ID ADI65088 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 582
ID ADI63587 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 583
ID ADH82001 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.

PN US2003207388-A1.
PD 08-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 584
ID ADH99902 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 585
ID ADH81449 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 586
ID ADM82618 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 587
ID ADN16017 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 588
ID ADN16646 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 589
ID ADN15465 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 590
ID ADN14913 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 591
ID ADC81175 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 592
ID ADD76623 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003100087-A1.
PD 29-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 593
ID ADD87987 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 594
ID ADD86391 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 595
ID ADE75839 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 596
ID ADE23415 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 597
ID ADE23967 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 598
ID ADE24610 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 599
ID ADD87435 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 600
ID ADE89301 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 601
ID ADE18440 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 602
ID ADE88749 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 603
ID ADE94769 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 604
ID ADE91180 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 605
ID ADF35355 standard; protein; 653 AA.
DE Human PRO1111 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 606
ID ADE95321 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 607
ID ADE93431 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 608
ID ADF35012 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 609
ID ADE92327 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 610
ID ADE90628 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;

RESULT 611
ID ADE91775 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 612
ID ADG11605 standard; protein; 653 AA.
DE Human PRO1111 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 613
ID ADG02354 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 614
ID ADG22140 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 615
ID ADG20210 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 616
ID ADF98116 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 617
ID ADG24333 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 618
ID ADF98687 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 619
ID ADG03518 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 620
ID ADE91775 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

ID ADF99239 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 621
ID ADG16824 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 622
ID ADG05283 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 623
ID ADG19550 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 624
ID ADG13387 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 625
ID ADG08444 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
FN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 626
ID ADG15614 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 627
ID ADF97012 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 628
ID ADG06197 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 629
ID ADG23781 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
FN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 630
ID ADG04070 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 631
ID ADG24971 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
FN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 632
ID ADG07268 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
FN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 633
ID ADG07820 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
FN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 634
ID ADG55315 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
FN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 635
ID ADG60979 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
FN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 636
ID ADG62083 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
FN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 637
ID ADG82284 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 638
ID ADG57523 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.

PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 639
ID ADG56971 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 640
ID ADG55867 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 641
ID ADG58627 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 642
ID ADG70993 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 643
ID ADG58075 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 644
ID ADG53659 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 645
ID ADG71545 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 646
ID ADG81732 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 647
ID ADH19475 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 648
ID ADH30694 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 649
ID ADH12061 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 650
ID ADG52483 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 651
ID ADG54211 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 652
ID ADG81180 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 653
ID ADG56419 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 654
ID ADH12685 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 655
ID ADH20968 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 656
ID ADG61531 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;

Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 657
ID ADH20008 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 658
ID ADH28618 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 659
ID ADG54763 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 660
ID ADG59803 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 661
ID ADI81227 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 662
ID ADG09970 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 663
ID ADI15441 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 664
ID ADG09318 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 665
ID ADI14773 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 666
ID ADI18368 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 667
ID ADJ63649 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 668
ID ADJ77544 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 669
ID ADJ65666 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 670
ID ADM27802 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 671
ID ADM42526 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 672
ID ADM28388 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 673
ID ADI95870 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 674
ID ADI96422 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 675

ID ADS23274 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 676
ID ADT03358 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 677
ID AD203409 standard; protein; 653 AA.
DE Human secreted/transmembrane PRO1111 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 9; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 678
ID AEA38492 standard; protein; 653 AA.
DE Human secreted/transmembrane protein, #132.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 9; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 679
ID AEA23332 standard; protein; 653 AA.
DE Tumor antigen of hematopoietic origin TAOH15.
PN WO2005049075-A2.
PD 02-JUN-2005.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 9; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 680
ID AEB14155 standard; protein; 653 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 438.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 10.5%; Score 330; DB 9; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 681
ID AEB6353 standard; protein; 653 AA.
DE Human PRO amino acid sequence, seq id 438.
PN US2005245730-A1.
PD 03-NOV-2005.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 9; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 682
ID AEF79019 standard; protein; 653 AA.

DE Human NAG14 polypeptide SEQ ID NO: 2.
PN US2006035826-A1.
PD 16-FEB-2006.
PA (LINJ/) LIN J C.
PA (ROSE/) ROSENTHAL A.
Query Match 10.5%; Score 330; DB 10; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 683
ID AEG58300 standard; protein; 653 AA.
DE Human PRO1111 polypeptide SEQ ID NO: 438.
PN US2006073568-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 10; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 684
ID AFI43945 standard; protein; 653 AA.
DE Human cancer-related PRO protein amino acid sequence - SEQ ID 438.
PN US2006040351-A1.
PD 23-FEB-2006.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 10.5%; Score 330; DB 10; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 685
ID AFI24028 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111, SEQ ID NO:438.
PN EPI672070-A2.
PD 21-JUN-2006.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 10; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 686
ID ABUI2069 standard; protein; 775 AA.
DE Human NOV15a CG92531-01 protein SEQ ID 58.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 10.5%; Score 329.5; DB 6; Length 775;
Best Local Similarity 26.0%; Pred. No. 3.2e-12;
RESULT 687
ID ABG98014 standard; protein; 649 AA.
DE Human leucine rich repeat domain protein associated protein #1.
PN WO200274959-A2.
PD 26-SEP-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 10.5%; Score 329; DB 5; Length 649;
Best Local Similarity 24.6%; Pred. No. 2.8e-12;
RESULT 688
ID ADS98753 standard; protein; 824 AA.
DE Protein factor discovery related human contig polypeptide, SEQ ID 1017.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
PA (DRMA/) DRMANAC R T.
Query Match 10.5%; Score 329; DB 8; Length 824;
Best Local Similarity 25.5%; Pred. No. 3.7e-12;
RESULT 689

ID ABG34079 standard; protein; 627 AA.
DE Human Pro peptide #51.
PN WO200224888-A2.
PD 28-MAR-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 5; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 690
ID ADA01368 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003068779-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 6; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 691
ID ADA43797 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003064474-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 6; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 692
ID ADA43565 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 6; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 693
ID ADA01240 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 6; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 694
ID ADA01124 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 695
ID ADA43681 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 696
ID ADA06943 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 697
ID ADA08431 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
ID ADB99724 standard; protein; 627 AA.
DE ADB99724 standard; protein; 627 AA.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 699
ID ADB87007 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 700
ID ADB66162 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 701
ID ADB99840 standard; protein; 627 AA.
DE Human PRO polypeptide SEQ ID 100.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 702
ID ADB99495 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003082731-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 703
ID ADB66046 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 704
ID ADC23444 standard; protein; 627 AA.
DE Human transmembrane PRO polypeptide (SeqID 100).
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 705
ID ADC26137 standard; protein; 627 AA.
DE Human PRO34192 protein.
PN US2003073194-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 706
ID ADE04964 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 707
ID ADE11270 standard; protein; 627 AA.
DE Human PRO polypeptide #50.

PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 708
ID AD882201 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 709
ID ADD95496 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003064473-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 710
ID ADE06426 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003073195-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 711
ID ADE38201 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119120-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 712
ID AD88317 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003073189-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 713
ID ADD90898 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003073188-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 714
ID ADF99453 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003078401-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 715
ID ADG06546 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003077742-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 716
ID ADG05497 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003077741-A1.

PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 717
ID ADG82498 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003077744-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 718
ID ADE51751 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104560-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 719
ID ADE51867 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104561-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 720
ID ADE37725 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104564-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 721
ID ADE37609 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 722
ID ADD95380 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 723
ID ADE38080 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 724
ID ADE76169 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003124665-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 725
ID ADE39492 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119117-A1.
PD 26-JUN-2003.

PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 726
ID ADE04296 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003096364-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 727
ID ADE39893 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138896-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 728
ID ADE19758 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 729
ID ADE77336 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003124666-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 730
ID ADE65444 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 731
ID ADE76053 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 732
ID ADE37964 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 733
ID ADE64574 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 734
ID ADE38909 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003096363-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 735
ID ADE51983 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 736
ID ADD91014 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 737
ID ADE38793 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003108996-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 738
ID ADE37493 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104563-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 739
ID ADE06309 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138898-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 740
ID ADD90169 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003138904-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 741
ID ADE38677 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 742
ID ADE39608 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119118-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 743
ID ADD89213 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138897-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;

RESULT 753

ID ADH38774 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
FN US2003119140-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 754

ID ADH29409 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
FN US2003119137-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 755

ID ADH23712 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
FN US2003119143-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 756

ID ADH27042 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
FN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 757

ID ADH38310 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
FN US2003119124-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 758

ID ADH26926 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
FN US2003119134-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 759

ID ADH38194 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
FN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 760

ID ADH38890 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
FN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 761

ID ADH23828 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
FN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 762

ID ADH38890 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
FN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;

ID ADH40203 standard; protein; 627 AA.
DE Human PRO34192 protein.
PN US2003119132-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 763
ID ADH40088 standard; protein; 627 AA.
DE Human PRO34192 protein.
PN US2003119133-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 764
ID ADH31410 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119138-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 765
ID ADH29288 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119136-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 766
ID ADH49503 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119127-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 767
ID ADH51967 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119125-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 768
ID ADH49822 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119128-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 769
ID ADH52423 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119130-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 770
ID ADH52539 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119129-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 771
ID ADH58536 standard; protein; 627 AA.

DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119121-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 772
ID ADH51851 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119126-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 773
ID ADH58412 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119122-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 774
ID ADI13609 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119131-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 775
ID ADK00865 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003186373-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 776
ID ADL08606 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003186372-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 777
ID AEG75266 standard; protein; 627 AA.
DE Human PRO34192 protein.
PN US2006073579-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 10; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 778
ID AEG74481 standard; protein; 627 AA.
DE Human PRO34192 protein SEQ ID NO:100.
PN US2006073553-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 10; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 779
ID AEG73353 standard; protein; 627 AA.
DE Human PRO34192 protein.
PN US2006073551-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 10; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 780
ID AEG74597 standard; protein; 627 AA.
DE Human PRO34192 polypeptide SEQ ID NO:100.

PN US2006073552-A1.
PD 06-APR-2006.
PA (GFTH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 10; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 781
ID AAU32870 standard; protein; 636 AA.
DE Novel human secreted protein #3361.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.4%; Score 327.5; DB 4; Length 636;
Best Local Similarity 24.2%; Pred. No. 3.4e-12;
RESULT 782
ID AB084499 standard; protein; 626 AA.
DE Mouse cancer-associated protein MP14-035.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.3%; Score 324; DB 8; Length 626;
Best Local Similarity 24.3%; Pred. No. 5.5e-12;
RESULT 783
ID AAG5805 standard; protein; 628 AA.
DE Human leucine-rich repeat (LRR) family member, 33395 polypeptide.
PN WO200172827-A2.
PD 04-OCT-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.3%; Score 324; DB 4; Length 628;
Best Local Similarity 24.1%; Pred. No. 5.6e-12;
RESULT 784
ID ADN95165 standard; protein; 810 AA.
DE Human BEC/LEC-related protein sequence SeqID87.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 10.3%; Score 322.5; DB 7; Length 810;
Best Local Similarity 22.0%; Pred. No. 9.3e-12;
RESULT 785
ID ABR58642 standard; protein; 811 AA.
DE Human cancer related protein SEQ ID NO:299.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIO TECHNOLOGY INC.
Query Match 10.3%; Score 322.5; DB 6; Length 811;
Best Local Similarity 22.0%; Pred. No. 9.3e-12;
RESULT 786
ID AAO23114 standard; protein; 811 AA.
DE KIAA0644 'human modifier of p53 pathway' protein.
PN WO2003035833-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 10.3%; Score 322.5; DB 6; Length 811;
Best Local Similarity 22.0%; Pred. No. 9.3e-12;
RESULT 787
ID ADN95110 standard; protein; 811 AA.
DE Human LEC protein sequence SeqID32.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 10.3%; Score 322.5; DB 7; Length 811;
Best Local Similarity 22.0%; Pred. No. 9.3e-12;
RESULT 788
ID ADQ21196 standard; protein; 811 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4016.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.3%; Score 322.5; DB 8; Length 811;
Best Local Similarity 22.0%; Pred. No. 9.3e-12;
RESULT 789
ID AEL77006 standard; protein; 811 AA.

DE Toll-like receptor/Interleukin-1 receptor 14 (TLR14) SEQ ID NO 1.
PN WO2006111946-A2.
PD 26-OCT-2006.
PA (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.
Query Match 10.3%; Score 322.5; DB 10; Length 811;
Best Local Similarity 22.0%; Pred. No. 9.3e-12;
RESULT 790
ID ADR45590 standard; protein; 605 AA.
DE Homologue of LRSG-1, baboon ALS.
PN US2004176296-A1.
PD 03-SEP-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.3%; Score 322; DB 8; Length 605;
Best Local Similarity 36.2%; Pred. No. 7.1e-12;
RESULT 791
ID AAG67523 standard; protein; 628 AA.
DE Amino acid sequence of a human secreted polypeptide.
PN WO200166690-A2.
PD 13-SEP-2001.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 10.2%; Score 321; DB 4; Length 628;
Best Local Similarity 23.9%; Pred. No. 8.6e-12;
RESULT 792
ID AAB84469 standard; protein; 628 AA.
DE Amino acid sequence of an interferon omega-1 like protein NOV2.
PN WO200142471-A2.
PD 14-JUN-2001.
PA (CURA-) CURAGEN CORP.
Query Match 10.2%; Score 321; DB 4; Length 628;
Best Local Similarity 23.9%; Pred. No. 8.6e-12;
RESULT 793
ID ABP69326 standard; protein; 628 AA.
DE Human polypeptide SEQ ID NO 1373.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 10.2%; Score 321; DB 5; Length 628;
Best Local Similarity 23.9%; Pred. No. 8.6e-12;
RESULT 794
ID ADF69107 standard; protein; 628 AA.
DE Human MP53 protein sequence SEQ ID NO:77.
PN WO2003083047-A2.
PD 09-OCT-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 10.2%; Score 321; DB 7; Length 628;
Best Local Similarity 23.9%; Pred. No. 8.6e-12;
RESULT 795
ID ADH71652 standard; protein; 628 AA.
DE Human protein of the invention NOV22a SEQ ID NO:548.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 10.2%; Score 321; DB 8; Length 628;
Best Local Similarity 23.9%; Pred. No. 8.6e-12;
RESULT 796
ID ADH71654 standard; protein; 628 AA.
DE Human protein of the invention NOV22b SEQ ID NO:550.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 10.2%; Score 321; DB 8; Length 628;
Best Local Similarity 23.9%; Pred. No. 8.6e-12;
RESULT 797
ID AB084502 standard; protein; 628 AA.
DE Human cancer-associated protein HP14-035.3.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.2%; Score 321; DB 8; Length 628;
Best Local Similarity 23.9%; Pred. No. 8.6e-12;
RESULT 798
ID AB084503 standard; protein; 628 AA.

DE Human cancer-associated protein HP14-035.4.
PN WO2004074320-A2.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.2%; Score 321; DB 8; Length 628;
Best Local Similarity 23.9%; Pred. No. 8.6e-12;
RESULT 799
ID ABO84501 standard; protein; 628 AA.
DE Human cancer-associated protein HP14-035.4.
PN WO2004074320-A2.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.2%; Score 321; DB 8; Length 628;
Best Local Similarity 23.9%; Pred. No. 8.6e-12;
RESULT 800
ID ABO70928 standard; protein; 762 AA.
DE Human LP341 protein.
PN WO2003029778-A2.
PA (ELIL) LILLY & CO ELI.
Query Match 10.2%; Score 321; DB 6; Length 762;
Best Local Similarity 25.5%; Pred. No. 1.1e-11;
RESULT 801
ID ADI36917 standard; protein; 797 AA.
DE Human LRR protein #12.
PN US2003220263-A1.
PA (FEDE) FEDER J N.
PN 27-NOV-2003.
PA (MINT) MINTIER G.
PA (RAMA) RAMANATHAN C S.
Query Match 10.2%; Score 321; DB 8; Length 797;
Best Local Similarity 25.5%; Pred. No. 1.1e-11;
RESULT 802
ID ADS98018 standard; protein; 803 AA.
DE Protein factor discovery related isolated human polypeptide, SEQ ID 282.
PN WO2004087874-A2.
PA (NUVE-) NUVELO INC.
PA (DRMA) DRMANAC R T.
Query Match 10.2%; Score 321; DB 8; Length 803;
Best Local Similarity 25.5%; Pred. No. 1.1e-11;
RESULT 803
ID AAY13349 standard; protein; 660 AA.
DE Amino acid sequence of protein PRO265.
PN WO9914328-A2.
PA 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 2; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 804
ID ADC78348 standard; protein; 660 AA.
DE Human PRO265 protein.
PN WO200015796-A2.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 3; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 805
ID AAB80217 standard; protein; 660 AA.
DE Human PRO265 protein.
PN WO200104311-A1.
PA 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 4; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 806
ID AAB31208 standard; protein; 660 AA.
DE Amino acid sequence of human polypeptide PRO265.
PN WO200077037-A2.
PA 21-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 4; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 807
ID AAU12346 standard; protein; 660 AA.
DE Human PRO265 polypeptide sequence.
PN WO200140466-A2.
PA 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 4; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 808
ID ABB84839 standard; protein; 660 AA.
DE Human PRO265 protein sequence SEQ ID NO:46.
PN WO200206090-A2.
PA 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 5; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 809
ID ABB95445 standard; protein; 660 AA.
DE Human angiogenesis related protein PRO265 SEQ ID NO: 46.
PN WO200208284-A2.
PA 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE) BAKER K P.
PA (FERR) FERRARA N.
PA (GERB) GERBER H.
PA (GERR) GERRITSEN M E.
PA (GODD) GODDARD A.
PA (GODO) GODOWSKI P J.
PA (GURN) GURNEY A L.
PA (HILL) HILLAN K J.
PA (MARS) MARSTERS S A.
PA (PANG) PAN J.
PA (PAON) PAONI N F.
PA (STEP) STEPHAN J F.
PA (WATA) WATANABE C K.
PA (WILL) WILLIAMS P M.
PA (WOOD) WOOD W I.
Query Match 10.2%; Score 320; DB 5; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 810
ID ASU71595 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2002146709-A1.
PA 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 811
ID ABO17790 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003032156-A1.
PA 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 812
ID ASU71450 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2002132659-A1.
PA 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 813
ID ABO25179 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003040014-A1.
PA 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 814
ID ASU81044 standard; protein; 660 AA.

DE Human cancer-associated protein HP14-035.4.
PN WO2004074320-A2.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.2%; Score 321; DB 8; Length 628;
Best Local Similarity 23.9%; Pred. No. 8.6e-12;
RESULT 799
ID ABO84501 standard; protein; 628 AA.
DE Human cancer-associated protein HP14-035.4.
PN WO2004074320-A2.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.2%; Score 321; DB 8; Length 628;
Best Local Similarity 23.9%; Pred. No. 8.6e-12;
RESULT 800
ID ABO70928 standard; protein; 762 AA.
DE Human LP341 protein.
PN WO2003029778-A2.
PA (ELIL) LILLY & CO ELI.
Query Match 10.2%; Score 321; DB 6; Length 762;
Best Local Similarity 25.5%; Pred. No. 1.1e-11;
RESULT 801
ID ADI36917 standard; protein; 797 AA.
DE Human LRR protein #12.
PN US2003220263-A1.
PA (FEDE) FEDER J N.
PN 27-NOV-2003.
PA (MINT) MINTIER G.
PA (RAMA) RAMANATHAN C S.
Query Match 10.2%; Score 321; DB 8; Length 797;
Best Local Similarity 25.5%; Pred. No. 1.1e-11;
RESULT 802
ID ADS98018 standard; protein; 803 AA.
DE Protein factor discovery related isolated human polypeptide, SEQ ID 282.
PN WO2004087874-A2.
PA (NUVE-) NUVELO INC.
PA (DRMA) DRMANAC R T.
Query Match 10.2%; Score 321; DB 8; Length 803;
Best Local Similarity 25.5%; Pred. No. 1.1e-11;
RESULT 803
ID AAY13349 standard; protein; 660 AA.
DE Amino acid sequence of protein PRO265.
PN WO9914328-A2.
PA 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 2; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 804
ID ADC78348 standard; protein; 660 AA.
DE Human PRO265 protein.
PN WO200015796-A2.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 3; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 805
ID AAB80217 standard; protein; 660 AA.
DE Human PRO265 protein.
PN WO200104311-A1.
PA 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 4; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 806
ID AAB31208 standard; protein; 660 AA.
DE Amino acid sequence of human polypeptide PRO265.
PN WO200077037-A2.
PA 21-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 4; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 807
ID AAU12346 standard; protein; 660 AA.
DE Human PRO265 polypeptide sequence.
PN WO200140466-A2.
PA 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 4; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 808
ID ABB84839 standard; protein; 660 AA.
DE Human PRO265 protein sequence SEQ ID NO:46.
PN WO200206090-A2.
PA 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 5; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 809
ID ABB95445 standard; protein; 660 AA.
DE Human angiogenesis related protein PRO265 SEQ ID NO: 46.
PN WO200208284-A2.
PA 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE) BAKER K P.
PA (FERR) FERRARA N.
PA (GERB) GERBER H.
PA (GERR) GERRITSEN M E.
PA (GODD) GODDARD A.
PA (GODO) GODOWSKI P J.
PA (GURN) GURNEY A L.
PA (HILL) HILLAN K J.
PA (MARS) MARSTERS S A.
PA (PANG) PAN J.
PA (PAON) PAONI N F.
PA (STEP) STEPHAN J F.
PA (WATA) WATANABE C K.
PA (WILL) WILLIAMS P M.
PA (WOOD) WOOD W I.
Query Match 10.2%; Score 320; DB 5; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 810
ID ASU71595 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2002146709-A1.
PA 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 811
ID ABO17790 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003032156-A1.
PA 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 812
ID ASU71450 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2002132659-A1.
PA 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 813
ID ABO25179 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003040014-A1.
PA 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 814
ID ASU81044 standard; protein; 660 AA.

DE Human PRO polypeptide #175.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 815
ID ABU71896 standard; protein; 660 AA.
DE Human secreted/transmembrane protein PRO265.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 816
ID ABO01779 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 817
ID ABU66744 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 818
ID ABU54352 standard; protein; 660 AA.
DE Human secreted/transmembrane protein PRO265.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 819
ID ABU67297 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 820
ID AAO23116 standard; protein; 660 AA.
DE FLRT2 'human modifier of p53 pathway' protein.
PN WO2003035833-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 821
ID ABO47367 standard; protein; 660 AA.
DE Human secreted/transmembrane polypeptide PRO265.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 822
ID ABUS9825 standard; protein; 660 AA.
DE Novel secreted and transmembrane protein PRO265.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 823
ID ABO25015 standard; protein; 660 AA.
DE Human secreted/transmembrane protein (PRO) #175.
PN US2003027143-A1.

PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 824
ID ABU64504 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 825
ID ABU72065 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 826
ID ABU67350 standard; protein; 660 AA.
DE Human secreted protein PRO265.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 827
ID ABU67166 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 828
ID ABO14870 standard; protein; 660 AA.
DE Human secreted / transmembrane polypeptide PRO265.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 829
ID ABU67020 standard; protein; 660 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 350.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 830
ID ABU69627 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 831
ID ABU79808 standard; protein; 660 AA.
DE Human secreted/transmembrane protein PRO265.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 832
ID ABO14809 standard; protein; 660 AA.
DE Human secreted / transmembrane polypeptide PRO265.
PN US2003027143-A1.

PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 833
ID ADA45869 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 834
ID ADA76300 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 835
ID ADB29233 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 836
ID ADA18950 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 837
ID ADA61573 standard; protein; 660 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 838
ID ADB19358 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 839
ID ADB27899 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 840
ID ADA86378 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 841
ID ADB15942 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003087350-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 842
ID ADA47728 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 843
ID ADA18089 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 844
ID ABO32761 standard; protein; 660 AA.
DE Human secreted/transmembrane protein PRO265.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 845
ID ADA67523 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 846
ID ADB30530 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 847
ID ADA85826 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 848
ID ADA97038 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 849
ID ADA79342 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 850
ID ADA87481 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 851
ID ADB1683 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 852
ID ABO34821 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 853
ID ADA16064 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 854
ID ADA91775 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 855
ID ADB14838 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 856
ID ADA47287 standard; protein; 660 AA.
DE Human secreted/transmembrane polypeptide PRO265.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 857
ID ADB18799 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 858
ID ADA94014 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 859
ID ADB19910 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 860
ID ADB13222 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 861
ID ABO43323 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 862
ID ADA74476 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 863
ID ADA42209 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 864
ID ADB24709 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 865
ID ADA82233 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 866
ID ADA75196 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 867
ID ADA85274 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 868
ID ADA84722 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;

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RESULT 869
ID ABO17499 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 870
ID ADB29978 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 871
ID ADA80506 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 872
ID ADA75748 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 873
ID ADA46973 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 874
ID ADB25269 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 875
ID ADA93445 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 876
ID ADB26795 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 877
ID ADB31082 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 878
ID ABO17499 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 879
ID ADB24157 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 880
ID ADA96486 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 881
ID ADA81058 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 882
ID ADA95934 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 883
ID ADB26243 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 884
ID ADB21728 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 885
ID ADA77507 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 886
ID ADB18247 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 887
ID ADA86930 standard; protein; 660 AA.
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DE Novel human secreted and transmembrane protein PRO265.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 888
ID ADA16488 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 889
ID ADA12917 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 890
ID ADA41785 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 891
ID ADA8033 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 892
ID ADA46421 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 893
ID ADA17132 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 894
ID ADA42635 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 895
ID ADB28451 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 896
ID ADB29003 standard; protein; 660 AA.
DE Human PRO polypeptide #175.

PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 897
ID ADA76955 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 898
ID ADA88585 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 899
ID ADA97590 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 900
ID ADB27347 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 901
ID ADB22280 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 902
ID ABO19866 standard; protein; 660 AA.
DE Human secreted/transmembrane protein PRO265.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 903
ID ABO17560 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 904
ID ADA66971 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 905
ID ADB22832 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 906
ID ADB23605 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 907
ID ADA92327 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 908
ID ADB15390 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 909
ID ADB38642 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 910
ID ADB38090 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 911
ID ADB66562 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 912
ID ADB89642 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 913
ID ADB90374 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 914
ID ADB77554 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;

Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 915
ID ADB39475 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 916
ID ADB74690 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 917
ID ADB47098 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 918
ID ADB86705 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 919
ID ADB77310 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 920
ID ADB34467 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 921
ID ADB35571 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 922
ID ADB33915 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 923
ID ADB35019 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;

RESULT 924
ID ADB36123 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 925
ID ADB46518 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 926
ID ADC28336 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 927
ID ADC39536 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 928
ID ADC40050 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 929
ID ADC18878 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 930
ID ADC34174 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 931
ID ADC29229 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 932
ID ADC28760 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 933
ID ADC60469 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 934
ID ADC19302 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 935
ID ADC33750 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 936
ID ADC12820 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 937
ID ADC50391 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 938
ID ADC71938 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 939
ID ADC59917 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 940
ID ADC52924 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 941
ID ADC57278 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 942
ID ADC60469 standard; protein; 660 AA.

DE Novel human secreted and transmembrane protein PRO265.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 943
ID ADC50944 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 944
ID ADC65471 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 945
ID ADC54569 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 946
ID ADC53530 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 947
ID ADC59053 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 948
ID ADC55931 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 949
ID ADC58501 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 950
ID ADC12272 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 951
ID ADC03175 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 952
ID ADC90167 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 953
ID ADC69586 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 954
ID ADC48475 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 955
ID ADD10004 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 956
ID ADD04579 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 957
ID ADC80535 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 958
ID ADD11042 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 959
ID ADD10335 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO polypeptide #23.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 960
ID ADC47923 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194771-A1.

PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 961
ID ADD04827 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 962
ID ADC79983 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 963
ID ADD11295 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO polypeptide #23.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 964
ID ADD09452 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 965
ID ADD03833 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 966
ID ADD03409 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 967
ID ADD41165 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 968
ID ADD52304 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 969
ID ADD53044 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194792-A1.
PD 16-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 970
ID ADD53596 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 971
ID ADD37088 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO polypeptide #23.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 972
ID ADD51752 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 973
ID ADD02551 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 974
ID ADD01985 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 975
ID ADD54167 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 976
ID ADD92484 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 977
ID ADD91380 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 978
ID ADE03994 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

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Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 979
ID ADE32291 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 980
ID ADE22223 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 981
ID ADD79447 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 982
ID ADE41983 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 983
ID ADE17800 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 984
ID ADD91932 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 985
ID ADE33395 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 986
ID ADE33947 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 987
ID ADD79999 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 988
ID ADD93036 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 989
ID ADE19456 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 990
ID ADE34661 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 991
ID ADE18904 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 992
ID ADE43100 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 993
ID ADD95889 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 994
ID ADE22775 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 995
ID ADD78893 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 996
ID ADE32843 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 997
ID ADD79999 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 998
ID ADD93036 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 999
ID ADE19456 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1000
ID ADE34661 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
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RESULT 997
ID ADE42535 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 998
ID ADE40863 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 999
ID ADE40863 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1000
ID ADE40863 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1001
ID ADE40662 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1002
ID ADE92791 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1003
ID ADG21500 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1004
ID ADG23141 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1005
ID ADF97476 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1006
ID ADE40863 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1007
ID ADG79988 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1008
ID ADG63796 standard; protein; 660 AA.
DE Human secreted/transmembrane polypeptide PRO265.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1009
ID ADH59144 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1010
ID ADH55280 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1011
ID ADH55832 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1012
ID ADI37923 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1013
ID ADI65000 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1014
ID ADI63499 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1015
ID ADH81913 standard; protein; 660 AA.
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DE Novel human secreted and transmembrane protein PRO265.
PN US2003207388-A1.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1016
ID ADH81361 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1017
ID ADJ26191 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1018
ID ADM82530 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1019
ID ADN15929 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1020
ID ADN16558 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1021
ID ADN15377 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1022
ID ADN14825 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1023
ID ADI64051 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1024
ID ADC81087 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.

PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1025
ID ADE79106 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1026
ID ADD76535 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1027
ID ADD87899 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1028
ID ADD86303 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1029
ID ADE79530 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1030
ID ADE75751 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1031
ID ADE73206 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1032
ID ADE41296 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO polypeptide #23.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1033
ID ADE23327 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003092108-A1.

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PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1034
ID ADE23879 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1035
ID ADE24522 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1036
ID ADE87347 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1037
ID ADE89213 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US200319062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1038
ID ADE41210 standard; protein; 660 AA.
DE Human secreted/transmembrane polypeptide PRO265.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1039
ID ADE73741 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1040
ID ADE18352 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1041
ID ADE8661 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1042
ID ADE99295 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1043
ID ADE94681 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1044
ID ADE91092 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1045
ID ADE95233 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1046
ID ADE93343 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1047
ID ADF34924 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1048
ID ADE98414 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1049
ID ADE92239 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1050
ID ADE90540 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1051
ID ADE91687 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
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Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1052
ID ADE98841 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1053
ID ADG40311 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1054
ID ADF73705 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1055
ID ADG02266 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1056
ID ADG22052 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1057
ID ADG20122 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1058
ID ADF98028 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1059
ID ADG24245 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1060

ID ADF98599 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1061
ID ADG03430 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1062
ID ADF99151 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1063
ID ADG16736 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1064
ID ADG05195 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1065
ID ADG19462 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1066
ID ADF73281 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1067
ID ADG13299 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1068
ID ADG08356 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1069
ID ADG15526 standard; protein; 660 AA.

DE Human PRO polypeptide #175.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1070
ID ADP96924 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1071
ID ADG06109 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1072
ID ADG23693 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1073
ID ADG03982 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1074
ID ADG24883 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1075
ID ADG07180 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1076
ID ADG07732 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1077
ID ADG55227 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1078
ID ADG60891 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.

PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1079
ID ADG61995 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1080
ID ADG92124 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1081
ID ADG82196 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1082
ID ADG57435 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1083
ID ADG56883 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1084
ID ADG55779 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1085
ID ADG58539 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1086
ID ADG70905 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1087
ID ADG92551 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003027146-A1.

PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1088
ID ADG57987 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1089
ID ADG53571 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1090
ID ADG71457 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1091
ID ADG81644 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207805-A1.
PD 06-NOV-2003.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1092
ID ADH30606 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1093
ID ADG63645 standard; protein; 660 AA.
DE Human secreted/transmembrane polypeptide PRO265.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1094
ID ADH11973 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1095
ID ADG52395 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1096
ID ADG54123 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1097
ID ADG81092 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1098
ID ADG56331 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1099
ID ADH12597 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1100
ID ADG61443 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1101
ID ADH28530 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1102
ID ADG54675 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1103
ID ADG59715 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1104
ID ADH20340 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1105
ID ADH43479 standard; protein; 660 AA.
DE Human PRO polypeptide #23.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1106
ID ADH43479 standard; protein; 660 AA.
DE Human PRO polypeptide #23.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1107
ID ADH43479 standard; protein; 660 AA.
DE Human PRO polypeptide #23.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.


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Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1122
ID ADM24995 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1123
ID ADJ63561 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1124
ID ADM29741 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1125
ID ADJ77456 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1126
ID ADK82824 standard; protein; 660 AA.
DE Human PRO polypeptide #23.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1127
ID ADJ65578 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1128
ID ADM27714 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1129
ID ADM42438 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1130
ID ADO06063 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1131
ID ADM28300 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1132
ID ADR10915 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1133
ID ADRI7824 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOVERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERE/) GERBER H.
PA (GERK/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1134
ID ADI95782 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1135
ID ADI96334 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1136
ID ADI65657 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1137
ID ADS74463 standard; protein; 660 AA.
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DE Human secreted/transmembrane protein #7.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
RESULT 1138
ID ADS32286 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH/) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
RESULT 1139
ID ADT03270 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH/) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
RESULT 1140
ID ADT03500 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH/) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
RESULT 1141
ID ADU06386 standard; protein; 660 AA.
DE Novel bronchial cancer-associated human protein SeqID610.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match
Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
RESULT 1142
ID AD203321 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO265 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH/) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 9; Length 660;
RESULT 1143
ID AEA37738 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH/) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 9; Length 660;
RESULT 1144
ID AEB14067 standard; protein; 660 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 350.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match
Best Local Similarity 10.2%; Score 320; DB 9; Length 660;
RESULT 1145
ID AED23772 standard; protein; 660 AA.
DE Human secreted protein PRO 265, SEQ ID 28.
PN US2005214904-A1.
PD 29-SEP-2005.
PA (GETH/) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 9; Length 660;
RESULT 1146
ID AED86265 standard; protein; 660 AA.
DE Human PRO amino acid sequence, seq id 350.
PN US2005245730-A1.
PD 03-NOV-2005.
PA (GETH/) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 9; Length 660;
RESULT 1147
ID ABE68941 standard; protein; 660 AA.
DE Fibromodulin homologous PRO265 protein, SEQ ID 28.
PN US6974689-B1.
PD 13-DEC-2005.
PA (GETH/) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 10; Length 660;
RESULT 1148
ID ARG58212 standard; protein; 660 AA.
DE Human PRO265 polypeptide SEQ ID NO: 350.
PN US2006073568-A1.
PD 06-APR-2006.
PA (GETH/) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 10; Length 660;
RESULT 1149
ID AEI43857 standard; protein; 660 AA.
DE Human cancer-related PRO protein amino acid sequence - SEQ ID 350.
PN US2006040351-A1.
PD 23-FEB-2006.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
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PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 10.2%; Score 320; DB 10; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1150
ID AEI23940 standard; protein; 660 AA.
DE Human secreted/transmembrane protein PRO265, SEQ ID NO:350.
PN EP1672070-A2.
PD 21-JUN-2006.
PA (GETH/) GENENTECH INC.
Query Match 10.2%; Score 320; DB 10; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1151
ID ADT77808 standard; protein; 452 AA.
DE Chimeric Nogo receptor polypeptide.
PN WO2004090103-A2.
PD 21-OCT-2004.
PA (UYRP/) UNIV ROCHESTER.
Query Match 10.2%; Score 318.5; DB 8; Length 452;
Best Local Similarity 27.3%; Pred. No. 8.4e-12;
RESULT 1152
ID ADT77802 standard; protein; 452 AA.
DE Chimeric Nogo receptor polypeptide.
PN WO2004090103-A2.
PD 21-OCT-2004.
PA (UYRP/) UNIV ROCHESTER.
Query Match 10.2%; Score 318.5; DB 8; Length 452;
Best Local Similarity 27.8%; Pred. No. 8.4e-12;
RESULT 1153
ID AEF79023 standard; protein; 648 AA.
DE Mouse NAG14 polypeptide SEQ ID NO: 6.
PN US2006035826-A1.
PD 16-FEB-2006.
PA (LINJ/) LIN J C.
PA (ROSE/) ROSENTHAL A.
Query Match 10.1%; Score 317.5; DB 10; Length 648;
Best Local Similarity 25.0%; Pred. No. 1.5e-11;
RESULT 1154
ID AAE13006 standard; protein; 713 AA.
DE Human leucine-rich repeat (LRR) family member protein.
PN WO200175105-A2.
PD 11-OCT-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.1%; Score 317.5; DB 4; Length 713;
Best Local Similarity 23.1%; Pred. No. 1.7e-11;
RESULT 1155
ID AAU91335 standard; protein; 713 AA.
DE Human novel secreted protein LP223(a).
PN WO200214358-A2.
PD 21-FEB-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 10.1%; Score 316.5; DB 5; Length 713;
Best Local Similarity 23.1%; Pred. No. 1.9e-11;
RESULT 1156
ID ABG97991 standard; protein; 713 AA.
DE Human nervous system leucine rich repeat protein (HLRRNS1) #2.
PN WO200274959-A2.
PD 26-SEP-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 10.1%; Score 316.5; DB 5; Length 713;
Best Local Similarity 23.1%; Pred. No. 1.9e-11;
RESULT 1157
ID ASU52381 standard; protein; 713 AA.
DE Human GPCR related protein NOV31a.

PN WO200279398-A2.
PD 10-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 10.1%; Score 316.5; DB 6; Length 713;
Best Local Similarity 23.1%; Pred. No. 1.9e-11;
RESULT 1158
ID AEI91171 standard; protein; 713 AA.
DE Novel human secreted protein, LP223(a).
PN US2006147945-A1.
PD 06-JUL-2006.
PA (EDMO/) EDMONDS B T.
PA (MICA/) MICANOVIC R.
PA (OUWW/) OU W.
PA (SUEW/) SU E W.
PA (TSCN/) TSCHANG S R.
PA (WANG/) WANG H.
Query Match 10.1%; Score 316.5; DB 10; Length 713;
Best Local Similarity 23.1%; Pred. No. 1.9e-11;
RESULT 1159
ID ADT77796 standard; protein; 474 AA.
DE Chimeric Nogo receptor polypeptide.
PN WO2004090103-A2.
PD 21-OCT-2004.
PA (UYRP) UNIV ROCHESTER.
Query Match 10.0%; Score 314.5; DB 8; Length 474;
Best Local Similarity 27.8%; Pred. No. 1.6e-11;
RESULT 1160
ID RAU91341 standard; protein; 656 AA.
DE Human novel secreted protein LP223(b).
PN WO200214358-A2.
PD 21-FEB-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 10.0%; Score 313.5; DB 5; Length 656;
Best Local Similarity 23.6%; Pred. No. 2.7e-11;
RESULT 1161
ID AEI91183 standard; protein; 656 AA.
DE Novel human secreted protein, LP223(b).
PN US2006147945-A1.
PD 06-JUL-2006.
PA (EDMO/) EDMONDS B T.
PA (MICA/) MICANOVIC R.
PA (OUWW/) OU W.
PA (SUEW/) SU E W.
PA (TSCN/) TSCHANG S R.
PA (WANG/) WANG H.
Query Match 10.0%; Score 313.5; DB 10; Length 656;
Best Local Similarity 23.6%; Pred. No. 2.7e-11;
RESULT 1162
ID ADL24097 standard; protein; 713 AA.
DE Human NOVX polypeptide #71.
PN US2004002120-A1.
PD 01-JAN-2004.
PA (KEKU/) KEKUDA R.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (PATT/) PATTURAJAN M.
PA (BURG/) BURGESS C E.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (MALY/) MALYANKAR U M.
PA (BOLD/) BOLDOG F L.
PA (GUOX/) GUO X.
PA (SHEN/) SHENOY S G.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAUFIER R J.
PA (MILL/) MILLER C E.
PA (CASW/) CASMAN S J.
PA (PENA/) PENNA C E A.
PA (GANG/) GANGOLLI E A.
PA (GUSE/) GUSEV V Y.
PA (SMIT/) SMITHSON G.

PA (ZERH/) ZERHUSEN B D.
PA (GERL/) GERLACH V.
PA (POCH/) POCHART P F.
PA (PERV/) FERNANDES E R.
PA (SHIM/) SHIMKETS R A.
PA (RAST/) RASTELLI L.
PA (SPAD/) SPADERNA S K.
PA (LARO/) LAROCHELLE W J.
PA (ZHON/) ZHONG M.
PA (KHRA/) KHRAMTSOV N V.
PA (VOSS/) VOSS E Z.
PA (HERR/) HERRMANN J L.
Query Match
Best Local Similarity 10.0%; Score 313.5; DB 8; Length 713;
RESULT 1163
ID AAE09437 standard; protein; 592 AA.
DE Human sbgrango79a protein.
PN WO200160850-A1.
PD 23-AUG-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match
Best Local Similarity 10.0%; Score 312; DB 4; Length 592;
RESULT 1164
ID AAE25351 standard; protein; 592 AA.
DE Human LP polypeptide, LP243.
PN WO200248361-A2.
PD 20-JUN-2002.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 10.0%; Score 312; DB 5; Length 592;
RESULT 1165
ID AAU91329 standard; protein; 592 AA.
DE Human novel secreted protein LP243(b).
PN WO200214358-A2.
PD 21-FEB-2002.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 10.0%; Score 312; DB 5; Length 592;
RESULT 1166
ID ABP60996 standard; protein; 592 AA.
DE Novel human protein. SEQ ID 83.
PN WO200250105-A1.
PD 27-JUN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match
Best Local Similarity 10.0%; Score 312; DB 5; Length 592;
RESULT 1167
ID AAU79167 standard; protein; 592 AA.
DE Human leucine-rich repeat proteins-like protein NOV4.
PN WO200214368-A2.
PD 21-FEB-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 10.0%; Score 312; DB 5; Length 592;
RESULT 1168
ID ABG74693 standard; protein; 592 AA.
DE Human CGDD protein 6803363CD1 SEQ ID 19.
PN WO2003014322-A2.
PD 20-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 10.0%; Score 312; DB 6; Length 592;
RESULT 1169
ID ADE03417 standard; protein; 592 AA.
DE Human immunoglobulin superfamily member BGS-2.
PN US2003195163-A1.
PD 16-OCT-2003.
PA (WUSS/) WU S.
PA (KRYST/) KRYSTEK S R.
PA (LEEL/) LEE L.
PA (FEDE/) FEDER J N.
PA (CHEN/) CHENG J D.
Query Match
Best Local Similarity 10.0%; Score 312; DB 7; Length 592;
RESULT 1170
ID ADU02709 standard; protein; 592 AA.
DE Novel human polypeptide seqid 1176.
PN WO2004093804-A2.
PD 04-NOV-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 10.0%; Score 312; DB 8; Length 592;
RESULT 1171
ID ASI9159 standard; protein; 592 AA.
DE Novel human secreted protein, LP243(b).
PN US2006147945-A1.
PD 08-JUL-2006.
PA (EDMO/) EDMONDS B T.
PA (MICA/) MICANOVIC R.
PA (OUWW/) OU W.
PA (SUEW/) SU E W.
PA (TSCH/) TSCHANG S R.
PA (WANG/) WANG H.
Query Match
Best Local Similarity 10.0%; Score 312; DB 10; Length 592;
RESULT 1172
ID ABG61770 standard; protein; 608 AA.
DE Novel leucine-rich protein.
PN WO200229058-A2.
PD 11-APR-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 10.0%; Score 312; DB 5; Length 608;
RESULT 1173
ID ABG97967 standard; protein; 634 AA.
DE Human nervous system leucine rich repeat protein (HLRRNS1) #1.
PN WO200274959-A2.
PD 26-SEP-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match
Best Local Similarity 9.9%; Score 311; DB 5; Length 634;
RESULT 1174
ID ABR55628 standard; protein; 420 AA.
DE Amino acid sequence of rat Nogo-66 receptor homologue NgrH1.
PN WO2003035687-A1.
PD 01-MAY-2003.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS PHARMA GMBH.
Query Match
Best Local Similarity 9.9%; Score 310.5; DB 6; Length 420;
RESULT 1175
ID ADT77788 standard; protein; 420 AA.
DE Rat Nogo receptor 2 polypeptide.
PN WO2004090103-A2.
PD 21-OCT-2004.
PA (UVRP) UNIV ROCHESTER.
Query Match
Best Local Similarity 9.9%; Score 310.5; DB 8; Length 420;
RESULT 1176
ID AAO23115 standard; protein; 674 AA.
DE FLRT1 'human modifier of p53 pathway' protein.
PN WO2003035833-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Query Match
Best Local Similarity 9.9%; Score 310.5; DB 6; Length 674;
RESULT 1177
ID ADH17606 standard; protein; 674 AA.
DE Human NOV19a protein - SEQ ID 296.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 9.9%; Score 310.5; DB 8; Length 674;

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Best Local Similarity 21.5%; Pred. No. 4.3e-11;
RESULT 1178
ID ADH17628 standard; protein; 674 AA.
DE Human NOV191 protein - SEQ ID 318.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%; Pred. No. 4.3e-11;
RESULT 1179
ID ADH17630 standard; protein; 674 AA.
DE Human NOV19m protein - SEQ ID 320.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%; Pred. No. 4.3e-11;
RESULT 1180
ID ADH17634 standard; protein; 674 AA.
DE Human NOV19o protein - SEQ ID 324.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%; Pred. No. 4.3e-11;
RESULT 1181
ID ADH17632 standard; protein; 674 AA.
DE Human NOV19n protein - SEQ ID 322.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%; Pred. No. 4.3e-11;
RESULT 1182
ID ABO27346 standard; protein; 585 AA.
DE Human secreted/transmembrane polypeptide PRO1865.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 585;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1183
ID ABO34232 standard; protein; 585 AA.
DE Human secreted/transmembrane polypeptide PRO 1865.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 585;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1184
ID AAU29215 standard; protein; 649 AA.
DE Human PRO polypeptide sequence #192.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 4; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1185
ID AAB70533 standard; protein; 649 AA.
DE Human PRO3 protein sequence SEQ ID NO:6.
PN WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 309; DB 4; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1186
ID AAB87591 standard; protein; 649 AA.
DE Human PRO1865.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 4; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1187
ID AEG95916 standard; protein; 649 AA.
DE Human secreted/transmembrane protein PRO1865.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 5; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1188
ID ABB4953 standard; protein; 649 AA.
DE Human PRO1865 protein sequence SEQ ID NO:274.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 5; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1189
ID ABP70109 standard; protein; 649 AA.
DE Human NOV27a.
PN WO200272771-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 309; DB 5; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1190
ID ABB95559 standard; protein; 649 AA.
DE Human angiogenesis related protein PRO1865 SEQ ID NO: 274.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH ) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 9.9%; Score 309; DB 5; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1191
ID ABU58591 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003027272-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1192
ID ABU88139 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032127-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1193
ID ABU84454 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032112-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1194
ID ABR66328 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027278-A1.
PD 06-FEB-2003.
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Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1195
ID ABR65718 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1196
ID ABU99658 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1197
ID ABU82897 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1198
ID ABU90018 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1199
ID ABR68267 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1200
ID ABU96320 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1201
ID ABU92751 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1202
ID ABO08828 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1203
ID ABO02880 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1204
ID ABR75034 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1205
ID ABR94796 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1206
ID ABU85769 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1207
ID ABU98929 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003031353-A1.
PD 16-JAN-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1208
ID ABU98144 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1209
ID ABU91850 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1210
ID ABU9543 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1211
ID ABU86384 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1212
ID ABU67597 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1213
ID ABU80625 standard; protein; 649 AA.
DE Human PRO protein #192.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1214
ID ABU90941 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;

Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1215
ID ABO34000 standard; protein; 649 AA.
DE Human secreted/transmembrane protein PRO1865.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1216
ID ABR9543 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1217
ID ABR98933 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1218
ID ABO16456 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1219
ID ABR92356 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1220
ID ABO18997 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1221
ID ABR78418 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1222
ID ABR72017 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1223
ID ABR85154 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1224
ID ABO00293 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match

Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1225
ID ABO11625 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1226
ID ABO2270 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1227
ID ABR8844 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1228
ID ABR3539 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1229
ID ABO6340 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1230
ID ABR59376 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1231
ID ABO09438 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1232
ID ABO19302 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1233
ID ABO11320 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1234
ID ABR66938 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1235

ID ABO16151 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1236
ID ABO13857 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1237
ID ABU71571 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1238
ID ABU65760 standard; protein; 649 AA.
DE Human secreted/transmembrane protein, SEQ ID 384.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1239
ID ABO07608 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1240
ID ABO03795 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1241
ID ABR67243 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1242
ID ABO15846 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1243
ID ABU56127 standard; protein; 649 AA.
DE Human secreted/transmembrane protein, PRO1865.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1244
ID ABU72352 standard; protein; 649 AA.
DE Human PRO polypeptide #66.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1245

ID ABU65455 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1246
ID ABU95400 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1247
ID ABU71303 standard; protein; 649 AA.
DE Human PRO1865 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1248
ID ABO07913 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1249
ID ABR70154 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1250
ID ABR69487 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1251
ID ABO01628 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1252
ID ASU81430 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1253
ID ABR60227 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1254
ID ABU91025 standard; protein; 649 AA.
DE Human PRO polypeptide #66.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1255

ID ABR67962 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003027269-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1256 22.3%; Pred. No. 5.2e-11;
ID ABR65350 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003027268-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1257 22.3%; Pred. No. 5.2e-11;
ID ABR68572 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003027274-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1258 22.3%; Pred. No. 5.2e-11;
ID ABR71984 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1259 22.3%; Pred. No. 5.2e-11;
ID ABU85464 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
FN US2003022295-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1260 22.3%; Pred. No. 5.2e-11;
ID ABU89154 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003022297-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1261 22.3%; Pred. No. 5.2e-11;
ID ABU83234 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003032105-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1262 22.3%; Pred. No. 5.2e-11;
ID ABU95090 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
FN US2003032123-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1263 22.3%; Pred. No. 5.2e-11;
ID ABU90638 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
FN US2003032108-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1264 22.3%; Pred. No. 5.2e-11;
ID ABU84149 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003032111-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1265 22.3%; Pred. No. 5.2e-11;
ID ABU93800 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.

PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1266 22.3%; Pred. No. 5.2e-11;
ID ABR65045 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003027263-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1267 22.3%; Pred. No. 5.2e-11;
ID ABR68877 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003027271-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1268 22.3%; Pred. No. 5.2e-11;
ID ABO06693 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1269 22.3%; Pred. No. 5.2e-11;
ID ABR99238 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003040068-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1270 22.3%; Pred. No. 5.2e-11;
ID ABU57122 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
FN US2003027280-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1271 22.3%; Pred. No. 5.2e-11;
ID ABU86074 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
FN US2003022300-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1272 22.3%; Pred. No. 5.2e-11;
ID ABU82361 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
FN US2003036136-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1273 22.3%; Pred. No. 5.2e-11;
ID ABU87372 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
FN US2003036138-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1274 22.3%; Pred. No. 5.2e-11;
ID ABU83844 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003032109-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1275 22.3%; Pred. No. 5.2e-11;
ID ABO08218 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
FN US2003040066-A1.
PD 27-FEB-2003.

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Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1276
ID ABU92541 standard; protein; 649 AA.
DE Human secreted/transmembrane protein PRO1865.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1277
ID ABU81929 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1278
ID ABU66093 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1279
ID ABU81211 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1280
ID ABR59922 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1281
ID ABU94110 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1282
ID ABU99963 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1283
ID ABR66633 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1284
ID ABR91051 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1285
ID ABO53325 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003027986-A1.
PD 06-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1286
ID ABU94478 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003017540-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1287
ID ABU79360 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1288
ID ABU86689 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1289
ID ABU86994 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1290
ID ABU94783 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1291
ID ABO04710 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1292
ID ABR70459 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1293
ID ABU98624 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1294
ID ABR66023 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1295
ID ABR64740 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
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Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1296
ID ABU79665 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032110-A1.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1297
ID ABU93056 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1298
ID ABU96015 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1299
ID ABU91235 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1300
ID ABU90328 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1301
ID ABO09743 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1302
ID ABO11015 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1303
ID ABR71069 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040089-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1304
ID ABU98328 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1305
ID ABU87677 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1306
ID ABU91545 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1307
ID ABU93333 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1308
ID ABU84759 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1309
ID ABR69849 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1310
ID ABU80226 standard; protein; 649 AA.
DE Human PRO protein #192.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1311
ID ABU82540 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1312
ID ABU93495 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1313
ID ABO10048 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1314
ID ABO09133 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1315
ID ABU96504 standard; protein; 649 AA.
DE Human PRO polypeptide #66.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1316
ID ABU96504 standard; protein; 649 AA.
DE Human PRO polypeptide #66.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1316
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ID ABU10701 standard; protein; 649 AA.
DE Human secreted/transmembrane protein #192.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;
RESULT 1317
ID ABU72174 standard; protein; 649 AA.
DE Human PRO polypeptide #66.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1318
ID ABU95710 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032115-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;
RESULT 1319
ID ABU96919 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032140-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;
RESULT 1320
ID ABR70764 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1321
ID ABO05115 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;
RESULT 1322
ID ABO08523 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044922-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1323
ID ABO05730 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032118-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;
RESULT 1324
ID ABR74119 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036135-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1325
ID ABR95711 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1326
ID ABR81008 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1327
ID ABR81313 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;
RESULT 1328
ID ABM01009 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1329
ID ABR88611 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003088743-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1330
ID ABM77432 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1331
ID ABO28916 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1332
ID ABO31661 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003088725-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1333
ID ABM08078 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1334
ID ABO40558 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
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RESULT 1335
ID ABO35983 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1336
ID ABO44122 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1337
ID ADA78136 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1338
ID ABR7696 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1339
ID ABO3185 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1340
ID ABR90441 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1341
ID ABR17355 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1342
ID ABR95101 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1343
ID ABR95406 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1344
ID ADB17189 standard; protein; 649 AA.
DE Human transmembrane PRO polypeptide (SeqID 132).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1345
ID ABO21644 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1346
ID ABR97908 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1347
ID ABR87696 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1348
ID ABR77737 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1349
ID ABR27967 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1350
ID ABR06248 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1351
ID ABR03754 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1352
ID ABR35205 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1353
ID ABR26442 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;

Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1354
ID ABO48224 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1355
ID ABR92966 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1356
ID ABO24727 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1357
ID ABR11738 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1358
ID ABO2839 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1359
ID ABR16135 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1360
ID ABO27696 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1361
ID ABR29187 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1362
ID ABR07163 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1363
ID ABR21257 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1364
ID ABR09603 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1365
ID ABO41473 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1366
ID ABO36288 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1367
ID ABO43817 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1368
ID ABR76517 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1369
ID ABR76213 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1370
ID ABR25832 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1371
ID ABR26137 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1372
ID ABO03490 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036127-A1.

PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1373
ID ABO02575 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1374
ID ABO44304 standard; protein; 649 AA.
DE Human secreted/transmembrane polypeptide PRO 1865.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1375
ID ABR90746 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1376
ID ABR73814 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1377
ID ABO17066 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1378
ID ABR94491 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1379
ID ABR75998 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1380
ID ABR71374 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1381
ID ABR93271 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1382
ID ABR93576 standard; protein; 649 AA.

DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1383
ID ABR88001 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1384
ID ABO28001 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1385
ID ABO30136 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1386
ID ABO33345 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1387
ID ABO05033 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1388
ID ABO08993 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1389
ID ABO36593 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1390
ID ABO35678 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1391
ID ABO39643 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.

PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1392
ID ABM10518 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1393
ID ABM12043 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1394
ID ABO52189 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1395
ID ABO52494 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1396
ID ADA19994 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1397
ID ABO23812 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1398
ID ADB17377 standard; protein; 649 AA.
DE Human transmembrane PRO polypeptide (SeqID 132).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1399
ID ABR97298 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1400
ID ABR87086 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1401
ID ABM1128 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1402
ID ABM28272 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1403
ID ABO32271 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1404
ID ABM15398 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1405
ID ABM06553 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1406
ID ABM04364 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1407
ID ABM22477 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1408
ID ABM07773 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1409
ID ABO40863 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1410
ID ABM35510 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1411
ID ABM33273 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1412
ID ABO52799 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1413
ID ABO50359 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1414
ID ABU93153 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1415
ID ABO44405 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1416
ID ABO06035 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1417
ID ABM18575 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1418
ID ABR97603 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1419
ID ABR80703 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.

PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1420
ID ABM01314 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1421
ID ABR88916 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1422
ID ABM13568 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1423
ID ABM20952 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1424
ID ABO42083 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1425
ID ABO42693 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1426
ID ABM10213 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1427
ID ABO38728 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1428
ID ABM32968 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073185-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1429
ID ABM22782 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1430
ID ABM74993 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1431
ID ADA79928 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1432
ID ABR96383 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1433
ID ABM02534 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1434
ID ABR86476 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1435
ID ABR86781 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1436
ID ABM16745 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1437
ID ABM29797 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1438
ID ABO29221 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003096359-A1.
PD 22-MAY-2003.

DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1439
ID ABM24002 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1440
ID ABM23392 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1441
ID ABM22172 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1442
ID ABO37813 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1443
ID ABM28577 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1444
ID ABM28577 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1445
ID ABM6526 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1446
ID ABM75908 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1447
ID ABM34188 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003096359-A1.
PD 22-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1448
ID ABR34493 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1449
ID ABO20424 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1450
ID ABO21339 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1451
ID ABO22254 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1452
ID ADA20166 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1453
ID ABR96688 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1454
ID ABR85866 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1455
ID ABR99848 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1456
ID ABR00399 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1457
ID ABO18387 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044920-A1.

ID ABR00704 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1458
ID ABO29831 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1459
ID ABR23697 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1460
ID ABR29492 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1461
ID ABO38423 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1462
ID ABO45723 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1463
ID ABR20647 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1464
ID ADA81655 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1465
ID ABO16761 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1466
ID ABO18387 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044920-A1.

PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1467
ID ABO22814 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1468
ID ABO23119 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1469
ID ABR92661 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1470
ID ABR81618 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1471
ID ABM78042 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1472
ID ABR89831 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1473
ID ABM26747 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1474
ID ABM13873 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1475
ID ABO28611 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1476
ID ABO48529 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.

ID ABO30441 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1477
ID ABM07468 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1478
ID ABM04059 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1479
ID ABO37203 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1480
ID ABO41778 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1481
ID ABO35373 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1482
ID ABM25222 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1483
ID ABO47614 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1484
ID ABO47919 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1485
ID ABO48529 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.

PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1486
ID ABO51579 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1487
ID ABO51884 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1488
ID ABO50664 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1489
ID ABR79788 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1490
ID ABR17050 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1491
ID ABO18082 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1492
ID ABO21034 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1493
ID ABR96993 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1494
ID ABR12348 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1495
ID ABR16440 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1496
ID ABR24307 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1497
ID ABR14788 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1498
ID ABR04669 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1499
ID ABR06858 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1500
ID ABR09298 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;

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GenCore version 6.2

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OM protein - protein search, using sw model

Run on: January 28, 2007, 17:25:31 ; Search time 52 Seconds

(without alignments)
1006.602 Million cell updates/sec

Title: US-10-677-669-69

Perfect score: 3135

Sequence: 1 MGRVPLLLPLLLLLALGPG.....PLMGPPGGLQSLHAKPYI 598

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

Issued Patents AA:*

1: /EMC_Celerra_SID33/ptodata/2/iaa/5 COMB.pep:*

2: /EMC_Celerra_SID33/ptodata/2/iaa/6 COMB.pep:*

3: /EMC_Celerra_SID33/ptodata/2/iaa/7 COMB.pep:*

4: /EMC_Celerra_SID33/ptodata/2/iaa/H COMB.pep:*

5: /EMC_Celerra_SID33/ptodata/2/iaa/pCTUS COMB.pep:*

6: /EMC_Celerra_SID33/ptodata/2/iaa/RE COMB.pep:*

7: /EMC_Celerra_SID33/ptodata/2/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
2	3135	100.0	598	2	US-09-944-457-69
7	3083.5	98.4	673	2	US-09-963-950-2
19	337	10.7	653	2	US-09-520-781-10
20	337	10.7	653	2	US-09-957-187-10
21	337	10.7	653	2	US-09-991-053-10
22	333	10.6	590	2	US-09-520-781-12
23	333	10.6	590	2	US-09-957-187-12
24	333	10.6	590	2	US-09-991-053-12
36	322	10.3	605	2	US-09-963-950-5
43	320	10.2	660	2	US-09-949-016-6843
55	320	10.2	660	2	US-09-689-486-58
57	320	10.2	663	2	US-09-973-424A-58
58	310.5	9.9	674	2	US-09-689-486-59
59	310.5	9.9	674	2	US-09-973-424A-59
61	310.5	9.9	674	2	US-09-973-424A-60
62	310.5	9.9	674	2	US-09-973-424A-75
63	310	9.9	662	2	US-08-949-016-10298
64	308	9.8	649	2	US-09-689-486-57
65	308	9.8	649	2	US-09-973-424A-57
66	307.5	9.8	674	2	US-09-949-016-7204
67	307.5	9.8	674	2	US-09-689-486-7
68	307.5	9.8	674	2	US-09-973-424A-7
69	305.5	9.7	664	2	US-09-973-424A-68
70	302	9.6	605	1	US-08-190-802A-49

71	302	9.6	605	2	US-08-477-346-49	Sequence 49, Appl
72	302	9.6	605	2	US-08-473-089-49	Sequence 49, Appl
73	302	9.6	605	2	US-08-487-072A-49	Sequence 49, Appl
74	302	9.6	605	2	US-09-538-092-1087	Sequence 1087, Ap
75	302	9.6	623	2	US-09-949-016-10995	Sequence 10995, A
76	301	9.6	448	2	US-09-520-781-32	Sequence 32, Appl
77	301	9.6	448	2	US-09-957-187-32	Sequence 32, Appl
78	301	9.6	448	2	US-09-991-053-32	Sequence 32, Appl
79	298.5	9.5	649	2	US-09-188-930-305	Sequence 305, App
80	298.5	9.5	649	2	US-09-312-283C-305	Sequence 305, App
126	284.5	9.1	745	2	US-10-104-047-2955	Sequence 2955, Ap
127	282.5	9.0	745	2	US-10-104-047-2960	Sequence 2960, Ap
128	281.5	9.0	603	1	US-08-190-802A-50	Sequence 50, Appl
129	281.5	9.0	603	2	US-08-477-346-50	Sequence 50, Appl
130	281.5	9.0	603	2	US-08-473-089-50	Sequence 50, Appl
131	281.5	9.0	603	2	US-08-487-072A-50	Sequence 50, Appl
132	271.5	8.7	353	2	US-08-986-485-6	Sequence 6, Appli
133	271.5	8.7	1504	2	US-10-037-417-98	Sequence 98, Appl
134	271	8.6	473	2	US-09-949-016-8448	Sequence 8448, Ap
142	259	8.3	610	1	US-07-821-717B-6	Sequence 6, Appli
143	259	8.3	610	1	US-08-119-928B-6	Sequence 6, Appli
144	259	8.3	610	1	US-08-135-929A-11	Sequence 11, Appl
145	259	8.3	610	1	US-08-234-265A-11	Sequence 11, Appl
146	258	8.2	1523	2	US-09-182-024A-2	Sequence 2, Appli
166	255.5	8.1	1480	2	US-09-191-647-7	Sequence 7, Appli
167	255.5	8.1	1480	2	US-09-540-245A-7	Sequence 7, Appli
168	255.5	8.1	1480	2	US-09-540-153-7	Sequence 7, Appli
169	255.5	8.1	1480	2	US-09-182-024A-5	Sequence 5, Appli
170	255.5	8.1	1480	2	US-10-289-776-7	Sequence 7, Appli
171	255.5	8.1	1480	5	PCR-US91-09055-2	Sequence 2, Appli
172	253	8.1	567	2	US-10-037-417-106	Sequence 106, App
173	252	8.0	566	2	US-09-775-803-12	Sequence 12, Appl
174	252	8.0	567	2	US-10-037-417-105	Sequence 105, App
175	251	8.0	622	2	US-10-188-495-48	Sequence 48, Appl
176	249.5	8.0	789	2	US-09-831-846-2	Sequence 2, Appli
177	248	7.9	481	2	US-09-853-753-2	Sequence 2, Appli
178	248	7.9	485	2	US-09-949-016-8704	Sequence 8704, Ap
179	247.5	7.9	1525	2	US-09-191-647-2	Sequence 2, Appli
180	247.5	7.9	1525	2	US-09-540-245A-2	Sequence 2, Appli
181	247.5	7.9	1525	2	US-09-540-153-2	Sequence 2, Appli
182	247.5	7.9	1525	2	US-10-289-776-2	Sequence 2, Appli
183	247.5	7.9	1529	2	US-10-188-495-67	Sequence 67, Appl
184	246.5	7.9	1529	2	US-09-312-283C-396	Sequence 396, App
185	244	7.8	708	2	US-09-131-648-2	Sequence 2, Appli
203	243.5	7.8	312	2	US-10-037-417-108	Sequence 108, App
204	242.5	7.7	545	3	US-10-114-270-38	Sequence 38, Appl
205	242.5	7.7	545	3	US-10-114-270-40	Sequence 40, Appl
206	241	7.7	380	2	US-09-461-325-161	Sequence 161, App
207	241	7.7	380	2	US-10-012-542-161	Sequence 161, App
208	241	7.7	380	2	US-08-592-500-2	Sequence 2, Appli
209	240	7.7	560	2	US-08-195-006-2	Sequence 2, Appli
210	240	7.7	560	2	US-09-063-950-4	Sequence 4, Appli
211	240	7.7	560	2	US-09-775-803-14	Sequence 14, Appl
212	240	7.7	560	2	PCR-US94-07644A-2	Sequence 2, Appli
213	240	7.7	560	5	PCR-US91-09055-3	Sequence 3, Appli
214	236.5	7.5	222	5	PCR-US91-09055-3	Sequence 3, Appli
215	236.5	7.5	231	2	US-08-986-485-7	Sequence 7, Appli
216	230.5	7.4	544	2	US-10-068-426-1	Sequence 1, Appli
217	227	7.2	568	2	US-09-673-245-14	Sequence 14, Appl
218	226.5	7.2	544	2	US-10-068-426-3	Sequence 3, Appli
219	226.5	7.2	557	2	US-10-037-417-95	Sequence 95, Appl
220	226.5	7.2	719	2	US-10-094-749-2001	Sequence 2001, Ap
221	225.5	7.2	544	2	US-10-068-426-2	Sequence 2, Appli
222	225	7.2	735	2	US-09-191-647-9	Sequence 9, Appli
223	225	7.2	735	2	US-09-540-245A-9	Sequence 9, Appli
224	225	7.2	735	2	US-09-540-153-9	Sequence 9, Appli
225	225	7.2	735	2	US-10-289-776-9	Sequence 9, Appli
226	222.5	7.1	536	2	US-09-538-092-992	Sequence 992, App
227	222	7.1	196	5	PCR-US91-09055-5	Sequence 5, Appli
228	222	7.1	498	2	US-10-188-495-51	Sequence 51, Appl
229	222	7.1	591	2	US-10-188-495-50	Sequence 50, Appl
230	221.5	7.1	557	2	US-10-037-417-94	Sequence 94, Appl
231	220.5	7.0	841	2	US-09-935-430-657	Sequence 657, App

232	220.5	7.0	841	2	US-09-964-956-2	Sequence 2, Appll	430	178	5.7	1049	2	US-09-954-987B-170	Sequence 170, App
233	218.5	7.0	359	2	US-09-949-016-9732	Sequence 9732, Ap	437	178	5.7	1052	2	US-09-949-016-11508	Sequence 11508, A
234	217.5	6.9	562	2	US-09-673-245-7	Sequence 7, Appll	438	177.5	5.7	1050	2	US-09-954-987B-175	Sequence 175, App
235	217.5	6.9	837	2	US-09-964-956-5	Sequence 5, Appll	439	176.5	5.6	522	2	US-10-104-047-2664	Sequence 2664, Ap
236	214.5	6.8	255	2	US-09-893-737-232	Sequence 232, App	440	175	5.6	368	7	5340934-2	Patent No. 5340934
237	212	6.8	531	2	US-10-068-426-6	Sequence 6, Appll	441	173.5	5.5	998	2	US-10-101-464A-914	Sequence 914, App
238	211	6.7	531	2	US-10-068-426-6	Sequence 6, Appll	442	172.5	5.5	282	1	US-08-442-063A-45	Sequence 45, Appl
239	210.5	6.7	4302	2	US-08-658-136-5	Sequence 5, Appll	443	172.5	5.5	307	1	US-08-442-063A-48	Sequence 48, Appl
240	210.5	6.7	4302	2	US-09-052-469-8	Sequence 8, Appll	444	172.5	5.5	333	1	US-08-442-063A-27	Sequence 27, Appl
241	210.5	6.7	4302	2	US-08-422-582-8	Sequence 8, Appll	445	172.5	5.5	338	2	US-09-689-486-63	Sequence 63, Appl
242	210.5	6.7	4302	2	US-09-052-462-8	Sequence 8, Appll	446	172.5	5.5	338	2	US-09-373-424A-63	Sequence 63, Appl
243	210.5	6.7	531	2	US-10-068-426-4	Sequence 4, Appll	447	172.5	5.5	342	1	US-08-272-919-2	Sequence 2, Appll
244	209	6.7	1091	2	US-08-986-485-5	Sequence 5, Appll	448	172.5	5.5	342	1	US-08-619-916-2	Sequence 2, Appll
245	208.5	6.7	424	2	US-09-949-016-7950	Sequence 7950, Ap	449	172.5	5.5	342	5	PCT-US95-08542-2	Sequence 4, Appll
246	207.5	6.6	415	2	US-09-935-430-659	Sequence 59, App	450	172.5	5.5	359	2	US-08-303-238-4	Sequence 4, Appll
247	207.5	6.6	440	2	US-09-964-956-29	Sequence 29, Appl	451	172.5	5.5	359	2	US-08-458-834-4	Sequence 4, Appll
248	207.5	6.6	798	2	US-09-935-430-658	Sequence 58, App	452	172.5	5.5	359	2	US-09-538-092-868	Sequence 868, App
249	207.5	6.6	798	2	US-09-964-956-28	Sequence 28, Appl	453	172.5	5.5	359	2	US-09-949-016-6143	Sequence 6143, Ap
250	206.5	6.6	1101	2	US-08-986-485-2	Sequence 2, Appll	454	172.5	5.5	360	2	US-09-949-016-7925	Sequence 7925, Ap
251	206	6.6	428	2	US-09-949-016-6625	Sequence 6625, Ap	455	172.5	5.5	1388	2	US-10-153-469A-10	Sequence 10, Appl
252	206	6.6	433	2	US-09-949-016-8521	Sequence 8521, Ap	456	172.5	5.5	1388	2	US-10-104-889-10	Sequence 10, Appl
253	205	6.5	4339	2	US-09-052-469-6	Sequence 6, Appll	457	170.5	5.4	373	2	US-09-724-864-43	Sequence 43, Appl
254	205	6.5	4339	2	US-08-422-582-6	Sequence 6, Appll	458	170	5.4	907	2	US-09-170-496B-264	Sequence 264, App
255	203.5	6.5	4339	2	US-09-052-462-6	Sequence 6, Appll	459	169.5	5.4	907	2	US-09-170-496B-278	Sequence 278, App
256	203.5	6.5	4303	1	US-08-460-751-2	Sequence 2, Appll	460	169.5	5.4	353	7	5340934-4	Patent No. 5340934
257	203.5	6.5	4303	2	US-09-479-467A-2	Sequence 2, Appll	461	168	5.4	1049	5	US-09-954-987B-172	Sequence 172, App
258	203.5	6.5	4303	2	US-09-655-160-2	Sequence 2, Appll	462	167	5.3	746	5	PCT-US95-10509-2	Sequence 2, Appll
259	201.5	6.4	606	2	US-10-094-749-2513	Sequence 2513, Ap	463	167	5.3	1112	2	US-09-353-585-3	Sequence 3, Appll
260	200.5	6.4	302	2	US-09-482-273-105	Sequence 105, App	464	166.5	5.3	284	2	US-09-482-273-174	Sequence 174, App
261	200.5	6.4	724	2	US-10-104-047-2224	Sequence 2224, Ap	465	166	5.3	835	3	US-09-396-985B-6	Sequence 6, Appll
262	199	6.3	321	2	US-10-104-047-2504	Sequence 2504, Ap	466	166	5.3	1112	2	US-09-353-585-2	Sequence 2, Appll
263	198.5	6.3	1338	2	US-09-631-603-2	Sequence 2, Appll	484	164.5	5.2	582	2	US-09-081-149-8	Sequence 8, Appll
264	196.5	6.3	716	2	US-09-312-283C-183	Sequence 183, App	485	164.5	5.2	584	2	US-09-949-016-10752	Sequence 10752, A
265	196.5	6.3	771	2	US-09-188-530-183	Sequence 183, App	486	164.5	5.2	858	2	US-10-104-047-2918	Sequence 2918, Ap
266	195.5	6.2	553	2	US-10-037-417-28	Sequence 28, Appl	504	164	5.2	904	2	US-09-949-002-352	Sequence 352, App
267	195.5	6.2	742	2	US-10-104-047-2807	Sequence 2807, Ap	505	164	5.2	910	2	US-09-949-002-483	Sequence 483, App
268	195	6.2	832	2	US-09-935-430-660	Sequence 660, App	506	163	5.2	582	2	US-09-081-149-7	Sequence 7, Appll
269	195	6.2	853	2	US-09-964-956-30	Sequence 30, Appl	507	163	5.2	753	2	US-09-056-383-13	Sequence 13, Appl
270	194.5	6.2	699	2	US-09-949-016-6073	Sequence 6073, Ap	508	161	5.1	559	2	US-09-081-149-2	Sequence 2, Appll
271	194.5	6.2	720	2	US-09-949-016-9819	Sequence 9819, Ap	509	160	5.1	942	2	US-10-101-464A-911	Sequence 911, App
272	193.5	6.2	224	5	PCT-US91-09055-4	Sequence 4, Appll	510	158.5	5.1	1032	2	US-09-954-987B-192	Sequence 192, App
273	193.5	6.2	542	2	US-10-037-417-97	Sequence 97, Appl	511	158	5.0	257	2	US-09-270-767-41554	Sequence 41554, A
274	193.5	6.0	301	2	US-10-068-426-9	Sequence 9, Appll	512	158	5.0	352	2	US-09-949-016-6781	Sequence 6781, Ap
275	189.5	5.9	196	5	PCT-US91-09055-6	Sequence 6, Appll	513	158	5.0	374	2	US-09-949-016-7689	Sequence 7689, Ap
276	186.5	5.9	799	3	US-09-396-985B-4	Sequence 4, Appll	514	157.5	5.0	236	1	US-08-442-063A-42	Sequence 42, Appl
277	186.5	5.9	839	3	US-09-396-985B-2	Sequence 2, Appll	515	157.5	5.0	622	2	US-09-949-002-522	Sequence 522, App
278	186.5	5.9	839	3	US-09-396-985B-98	Sequence 98, Appl	516	157	5.0	786	2	US-10-104-047-2293	Sequence 2293, Ap
279	186.5	5.9	844	2	US-09-949-016-9438	Sequence 9438, Ap	517	156.5	5.0	376	2	US-09-538-092-1276	Sequence 1276, Ap
280	186	5.9	451	2	US-09-538-092-999	Sequence 999, App	518	156	5.0	975	2	US-09-949-016-7595	Sequence 7595, Ap
281	185	5.9	451	2	US-09-949-016-9282	Sequence 9282, Ap	520	155	4.9	1041	2	US-09-954-987B-184	Sequence 184, App
282	184	5.9	302	2	US-10-068-426-7	Sequence 7, Appll	521	155	4.9	1059	2	US-09-954-987B-187	Sequence 187, App
283	184	5.9	320	1	US-07-613-083B-1	Sequence 1, Appll	528	155	4.9	377	2	US-09-949-016-7949	Sequence 7949, Ap
284	184	5.9	368	2	US-09-949-016-6115	Sequence 6115, Ap	529	154.5	4.9	1495	2	US-08-522-726B-1	Sequence 1, Appll
285	184	5.9	368	2	US-09-715-836A-9	Sequence 9, Appll	530	154.5	4.9	894	1	US-08-372-892-2	Sequence 2, Appll
286	184	5.9	382	2	US-09-949-016-10542	Sequence 10542, A	531	154.5	4.9	894	1	US-08-372-892-2	Sequence 2, Appll
287	184	5.8	662	2	US-09-538-092-1325	Sequence 1325, Ap	532	153.5	4.9	894	1	US-08-445-461-34	Sequence 34, Appl
288	183	5.8	662	2	US-09-949-016-6619	Sequence 6619, Ap	533	153.5	4.9	894	1	US-08-445-461-34	Sequence 34, Appl
289	183	5.8	662	2	US-09-949-016-10710	Sequence 10710, A	534	153.5	4.9	894	2	US-08-447-314-34	Sequence 34, Appl
290	183	5.8	379	2	US-09-944-457-2	Sequence 2, Appll	535	153.5	4.9	894	2	US-08-445-461-34	Sequence 34, Appl
291	182.5	5.8	958	2	US-09-706-594-5	Sequence 5, Appll	536	153.5	4.9	894	2	US-09-223-490-34	Sequence 34, Appl
292	182.5	5.8	966	2	US-09-964-956-32	Sequence 32, Appl	537	153.5	4.9	894	2	US-10-646-760-34	Sequence 34, Appl
293	182	5.8	378	2	US-09-689-426-62	Sequence 62, Appl	538	153.5	4.9	894	3	US-10-954-987B-6	Sequence 6, Appll
294	182	5.8	378	2	US-09-773-424A-62	Sequence 62, Appl	539	153.5	4.9	1032	2	US-09-954-987B-6	Sequence 6, Appll
295	180	5.7	493	2	US-10-037-417-30	Sequence 30, Appl	540	153	4.9	679	2	US-09-252-991A-18857	Sequence 18857, A
296	180	5.7	989	2	US-09-954-987B-171	Sequence 171, App	541	153	4.9	699	2	US-10-237-551-143	Sequence 143, App
297	179.5	5.7	515	3	US-10-162-335-92	Sequence 92, Appl	542	153	4.9	699	2	US-10-237-551-254	Sequence 254, App
298	179	5.7	290	2	US-10-068-426-10	Sequence 10, Appl	543	153	4.9	1248	2	US-10-042-810-2	Sequence 2, Appll
299	179	5.7	290	2	US-10-068-426-11	Sequence 11, Appl	544	153	4.9	1278	2	US-10-042-810-4	Sequence 4, Appll
300	179	5.7	290	2	US-10-068-426-12	Sequence 12, Appl	545	152.5	4.9	364	2	US-10-104-047-2127	Sequence 2127, Ap
301	179	5.7	302	2	US-10-068-426-8	Sequence 8, Appll	546	152	4.8	786	2	US-09-949-002-351	Sequence 351, App
302	178	5.7	368	1	US-08-303-238-3	Sequence 3, Appll	547	152	4.8	786	2	US-09-949-002-386	Sequence 386, App
303	178	5.7	368	2	US-08-458-834-3	Sequence 3, Appll	548	152	4.8	802	2	US-09-949-002-512	Sequence 512, App
304	178	5.7	522	2	US-10-094-749-2689	Sequence 2689, Ap	549	151.5	4.8	455	2	US-10-188-495-3	Sequence 3, Appll

550	151.5	4.8	1964	2	US-09-467-997-1	Sequence 1, Appli	651	136	4.3	692	2	US-09-461-657B-6	Sequence 6, Appli
551	151	4.8	832	2	US-09-270-767-46234	Sequence 46234, A	652	135.5	4.3	536	2	US-09-252-991A-31124	Sequence 31124, A
552	151	4.8	535	3	US-09-396-985B-99	Sequence 99, Appl	653	135.5	4.3	743	2	US-09-771-161A-164	Sequence 164, App
553	151	4.8	835	3	US-09-396-985B-104	Sequence 104, App	654	135.5	4.3	743	2	US-09-771-161A-254	Sequence 254, App
554	150.5	4.8	695	1	US-08-487-886-2	Sequence 2, Appli	655	135	4.3	446	2	US-10-101-464A-733	Sequence 733, App
555	150.5	4.8	695	2	US-08-482-855-2	Sequence 2, Appli	656	135	4.3	538	2	US-09-616-289-43	Sequence 43, Appl
556	150.5	4.8	695	2	US-08-474-862-2	GENERAL INFORMA	657	135	4.3	538	2	US-09-976-740-43	Sequence 43, Appl
574	150	4.8	513	2	US-09-068-804-14	Sequence 14, Appl	658	135	4.3	696	2	US-10-094-749-2425	Sequence 2425, Ap
575	149	4.8	1012	1	US-10-037-417-104	Sequence 104, App	659	135	4.3	723	2	US-09-434-408-2	Sequence 2, Appli
576	149	4.8	1012	1	US-08-475-891A-4	Sequence 4, Appli	660	135	4.3	723	2	US-10-104-047-2572	Sequence 2, Appli
577	149	4.8	1025	1	US-08-567-375-4	Sequence 4, Appli	661	135	4.3	907	2	US-08-783-774-2	Sequence 2, Appli
578	149	4.8	1025	1	US-08-587-680A-4	Sequence 4, Appli	662	135	4.3	907	2	US-09-328-599A-1	Sequence 1, Appli
579	149	4.8	1026	1	US-09-623-551-18	Sequence 18, Appl	663	135	4.3	907	5	PCT-US95-04611A-19	Sequence 19, Appl
580	149	4.8	1504	2	US-09-364-206-2	Sequence 2, Appli	664	134.5	4.3	802	2	US-09-823-240A-2	Sequence 2, Appli
581	149	4.8	1874	2	US-09-331-403-2	Sequence 2, Appli	665	134	4.3	536	2	US-09-292-225-21	Sequence 21, Appl
582	148.5	4.7	375	1	US-08-303-238-2	Sequence 2, Appli	666	134	4.3	550	2	US-09-616-289-47	Sequence 47, Appl
583	148.5	4.7	375	2	US-08-458-834-2	Sequence 2, Appli	667	134	4.3	550	2	US-09-976-740-47	Sequence 47, Appl
584	147.5	4.7	570	2	US-09-565-501A-104	Sequence 104, App	668	134	4.3	555	2	US-09-292-225-15	Sequence 15, Appl
585	147.5	4.7	570	2	US-09-639-206A-104	Sequence 104, App	669	134	4.3	555	2	US-09-292-225-18	Sequence 18, Appl
586	147.5	4.7	570	2	US-09-874-923-104	Sequence 104, App	670	133.5	4.3	1166	2	US-10-101-464A-900	Sequence 900, App
587	147.5	4.7	1728	2	US-09-949-002-532	Sequence 532, App	671	133	4.2	652	2	US-10-104-047-3364	Sequence 3364, Ap
588	147	4.7	177	2	US-09-270-767-32705	Sequence 32705, A	672	133	4.2	4391	2	US-10-006-011A-2	Sequence 2, Appli
589	147	4.7	177	2	US-09-270-767-47922	Sequence 47922, A	673	132.5	4.2	390	2	US-08-460-576-2	Sequence 2, Appli
590	147	4.7	265	2	US-09-270-767-45056	Sequence 45056, A	674	132.5	4.2	463	1	US-08-162-402B-9	Sequence 9, Appli
591	147	4.7	2414	1	US-08-227-536-2	Sequence 2, Appli	675	132.5	4.2	579	2	US-09-325-932A-185	Sequence 185, App
592	147	4.7	2414	2	US-09-538-092-1289	Sequence 1289, Ap	676	132.5	4.2	583	2	US-09-641-612-2	Sequence 2, Appli
593	147	4.7	2414	5	PCT-US95-0468A-2	Sequence 2, Appli	677	132.5	4.2	2035	1	US-08-046-585-5	Sequence 5, Appli
594	146.5	4.7	325	2	US-10-104-047-1320	Sequence 320, Ap	678	132.5	4.2	2035	5	US-08-393-703-5	Sequence 5, Appli
595	146.5	4.7	344	2	US-10-104-047-1320	Sequence 3, Appli	679	132.5	4.2	2035	5	PCT-US93-11721-5	Sequence 5, Appli
596	146.5	4.7	1404	1	US-08-400-159-2	Sequence 2, Appli	680	132.5	4.2	2045	2	US-09-949-016-10491	Sequence 10491, A
597	146.5	4.7	1404	2	US-08-611-729A-2	Sequence 2, Appli	681	132.5	4.2	3122	2	US-10-237-551-201	Sequence 201, App
598	146.5	4.7	1404	2	US-09-195-524-2	Sequence 2, Appli	682	132.5	4.2	3122	2	US-10-237-551-250	Sequence 250, App
599	146	4.7	786	2	US-09-103-429A-3	Sequence 3, Appli	683	132	4.2	287	2	US-09-893-737-110	Sequence 110, App
600	146	4.7	788	2	US-09-294-663-3	Sequence 3, Appli	684	132	4.2	465	1	US-08-162-402B-8	Sequence 8, Appli
601	146	4.7	885	1	US-08-372-892-4	Sequence 4, Appli	685	132	4.2	705	2	US-10-101-464A-894	Sequence 894, App
602	146	4.7	885	2	US-09-919-497-52	Sequence 52, Appl	686	132	4.2	979	2	US-08-514-213A-2	Sequence 2, Appli
603	145.5	4.6	2142	2	US-09-538-092-1142	Sequence 1142, Ap	687	132	4.2	979	2	US-09-015-399-5	Sequence 5, Appli
604	145.5	4.6	2142	2	US-09-949-002-371	Sequence 371, App	688	132	4.2	1003	2	US-09-949-016-11260	Sequence 11260, A
605	145	4.6	353	2	US-09-949-016-7923	Sequence 7923, Ap	689	131.5	4.2	461	2	US-10-037-417-96	Sequence 96, Appl
606	145	4.6	1032	2	US-09-954-987B-3	Sequence 3, Appli	690	131.5	4.2	571	2	US-09-252-991A-30533	Sequence 30533, A
607	144	4.6	661	1	US-08-514-014-4	Sequence 4, Appli	691	131	4.2	180	2	US-08-986-485-8	Sequence 8, Appli
608	144	4.6	661	1	US-08-833-823-4	Sequence 4, Appli	692	131	4.2	227	2	US-10-101-464A-666	Sequence 666, App
609	143.5	4.6	1274	4	US-09-294-663-4	Sequence 4, Appli	693	131	4.2	279	2	US-09-270-767-41558	Sequence 41558, A
610	143.5	4.6	1636	3	US-10-433-794-1	Sequence 1, Appli	694	131	4.2	407	2	US-09-180-439-6	Sequence 46649, A
611	143	4.6	935	2	US-09-477-962-107	Sequence 107, App	695	131	4.2	799	2	US-09-328-986-73	Sequence 73, Appl
612	142.5	4.5	141	2	US-09-270-767-31706	Sequence 31706, A	696	131	4.2	947	2	US-09-228-986-73	Sequence 73, Appl
613	142.5	4.5	141	2	US-09-270-767-46923	Sequence 46923, A	697	131	4.2	947	2	US-10-101-464A-73	Sequence 73, Appl
614	142.5	4.5	805	2	US-09-103-429A-4	Sequence 4, Appli	698	131	4.2	1062	2	US-09-802-540-16313	Sequence 16313, A
615	142.5	4.5	805	2	US-09-294-663-4	Sequence 4, Appli	699	131	4.2	1196	2	US-08-881-706-2	Sequence 2, Appli
616	142	4.5	326	2	US-09-689-486-64	Sequence 64, Appl	700	131	4.2	1196	2	US-09-823-394-2	Sequence 2, Appli
617	142	4.5	326	2	US-09-973-424A-64	Sequence 64, Appl	701	131	4.2	1938	2	US-09-949-016-6609	Sequence 6609, Ap
618	142	4.5	363	2	US-10-188-495-6	Sequence 6, Appli	702	130.5	4.2	843	2	US-10-101-464A-893	Sequence 893, App
619	142	4.5	365	2	US-10-101-464A-901	Sequence 901, App	703	130.5	4.2	878	2	US-09-556-706B-2	Sequence 2, Appli
620	142	4.5	435	2	US-10-188-495-5	Sequence 5, Appli	704	130.5	4.2	878	2	US-09-724-418A-2	Sequence 2, Appli
621	142	4.5	661	2	US-10-037-417-107	Sequence 107, App	705	130.5	4.2	3729	1	US-08-804-227C-4	Sequence 4, Appli
622	140.5	4.5	345	2	US-10-101-464A-802	Sequence 802, App	706	130	4.1	619	2	US-10-037-417-34	Sequence 34, Appl
623	140.5	4.5	376	1	US-08-303-238-1	Sequence 1, Appli	707	130	4.1	645	2	US-10-101-464A-920	Sequence 920, App
624	140.5	4.5	376	2	US-08-458-834-1	Sequence 1, Appli	708	129.5	4.1	550	2	US-09-252-991A-21295	Sequence 21295, A
625	140	4.5	283	2	US-09-949-016-7910	Sequence 7910, Ap	709	129.5	4.1	912	5	PCT-US95-03747-2	Sequence 2, Appli
626	140	4.5	547	2	US-10-101-464A-928	Sequence 928, App	710	129.5	4.1	1251	3	US-10-114-270-80	Sequence 80, Appl
627	139	4.4	5179	2	US-09-538-092-1258	Sequence 1258, Ap	711	129	4.1	363	2	US-09-270-767-44030	Sequence 44030, A
628	138.5	4.4	710	2	US-10-104-047-3402	Sequence 3402, Ap	712	129	4.1	883	2	US-09-252-991A-23655	Sequence 23655, A
640	138	4.4	323	2	US-09-949-016-7924	Sequence 7924, Ap	713	129	4.1	895	2	US-09-252-991A-26129	Sequence 26129, A
641	138	4.4	1003	2	US-10-094-749-2528	Sequence 2528, Ap	714	129	4.1	1133	2	US-10-101-464A-809	Sequence 809, App
642	137.5	4.4	141	2	US-09-270-767-45511	Sequence 45511, A	715	129	4.1	1940	1	US-08-644-271-30	Sequence 30, Appl
643	137.5	4.4	884	7	5208144-8	Patent No. 5208144	716	129	4.1	1940	2	US-09-077-355-34	Sequence 34, Appl
644	137	4.4	4544	1	US-08-469-486-52	Sequence 52, Appl	717	129	4.1	1940	2	US-10-016-283-34	Sequence 2, Appli
645	137	4.4	4544	1	US-08-469-658-52	Sequence 52, Appl	718	129	4.1	2321	2	US-09-230-652-2	Sequence 2, Appli
646	136.5	4.4	984	2	US-10-101-464A-919	Sequence 919, App	719	129	4.1	2321	1	US-09-612-226B-2	Sequence 2, Appli
647	136.5	4.4	2972	2	US-09-579-181-2	Sequence 2, Appli	720	128.5	4.1	188	1	US-08-442-063A-39	Sequence 39, Appl
648	136.5	4.4	3118	2	US-09-579-181-1	Sequence 1, Appli	721	128.5	4.1	466	1	US-08-836-854-15	Sequence 15, Appl
649	136	4.3	287	2	US-10-104-047-3292	Sequence 3292, Ap	722	128.5	4.1	508	2	US-10-104-047-3233	Sequence 3233, Ap
650	136	4.3	692	2	US-07-757-342D-6	Sequence 6, Appli	723	128.5	4.1	653	2	US-10-101-464A-953	Sequence 953, App

724	128.5	4.1	864	2	US-10-101-464A-896	Sequence 896, App	844	123	3.9	557	2	US-09-248-796A-26892	Sequence 26892, A
725	128.5	4.1	865	2	US-09-902-540-10416	Sequence 10416, A	845	123	3.9	888	1	US-08-445-640-35	Sequence 35, Appl
726	128.5	4.1	1023	1	US-08-475-591A-2	Sequence 2, Appl	846	123	3.9	888	2	US-08-170-558-35	Sequence 35, Appl
727	128.5	4.1	1023	1	US-08-567-375-2	Sequence 2, Appl	847	123	3.9	888	2	US-08-447-314-35	Sequence 35, Appl
728	128.5	4.1	1023	1	US-08-587-680A-2	Sequence 2, Appl	848	123	3.9	888	2	US-08-445-461-35	Sequence 35, Appl
729	128	4.1	475	2	US-09-252-991A-30242	Sequence 30242, A	849	123	3.9	888	2	US-09-223-490-35	Sequence 35, Appl
730	128	4.1	538	1	US-08-541-759B-2	Sequence 2, Appl	850	123	3.9	888	3	US-10-646-760-35	Sequence 28, Appl
731	128	4.1	717	2	US-10-101-464A-810	Sequence 810, App	851	123	3.9	924	1	US-08-481-130-28	Sequence 28, Appl
732	127.5	4.1	1006	2	US-10-415-147-12	Sequence 12, Appl	852	123	3.9	924	1	US-08-556-984A-28	Sequence 28, Appl
733	127.5	4.1	1006	2	US-10-114-270-8A	Sequence 8A, Appl	853	123	3.9	924	1	US-08-485-604-28	Sequence 28, Appl
734	127.5	4.1	1522	3	US-10-144-198-31	Sequence 31, Appl	854	123	3.9	924	1	US-08-487-595-28	Sequence 28, Appl
735	127.5	4.1	1581	2	US-09-949-002-414	Sequence 414, App	855	122.5	3.9	335	3	US-10-114-270-34	Sequence 34, Appl
736	127.5	4.1	3969	2	US-08-061-376-5	Sequence 5, Appl	856	122.5	3.9	335	3	US-10-114-270-36	Sequence 36, Appl
737	127.5	4.1	3969	2	US-09-538-092-1262	Sequence 1262, App	857	122.5	3.9	494	2	US-09-248-796A-16546	Sequence 16546, A
738	127	4.1	260	2	US-09-270-767-32658	Sequence 32658, A	858	122.5	3.9	595	2	US-09-641-612-5	Sequence 5, Appl
739	127	4.1	615	2	US-09-252-991A-26695	Sequence 26695, A	859	122.5	3.9	596	2	US-09-252-991A-18875	Sequence 18875, A
740	126.5	4.0	141	2	US-09-270-767-32244	Sequence 32244, A	860	122.5	3.9	968	2	US-09-180-439-3	Sequence 3, Appl
741	126.5	4.0	141	2	US-09-270-767-47461	Sequence 47461, A	861	122.5	3.9	968	2	US-09-180-439-4	Sequence 4, Appl
753	126.5	4.0	659	2	US-09-423-753-3	Sequence 3, Appl	862	122.5	3.9	1016	2	US-09-180-439-8	Sequence 8, Appl
754	126.5	4.0	659	3	US-10-241-476-3	Sequence 3, Appl	863	122.5	3.9	1036	2	US-09-771-161A-255	Sequence 255, App
755	126.5	4.0	685	2	US-08-872-855-2	Sequence 2, Appl	864	122.5	3.9	1036	2	US-09-771-161A-256	Sequence 256, App
756	126.5	4.0	685	2	US-09-423-753-25	Sequence 25, Appl	865	122	3.9	131	2	US-09-461-325-186	Sequence 186, App
757	126.5	4.0	685	2	US-09-641-612-7	Sequence 7, Appl	866	122	3.9	131	2	US-10-012-542-186	Sequence 186, App
758	126.5	4.0	685	3	US-10-241-476-25	Sequence 25, Appl	867	122	3.9	191	2	US-10-115-123-186	Sequence 186, App
759	126.5	4.0	919	2	US-10-101-464A-642	Sequence 642, App	868	122	3.9	206	2	US-09-461-325-412	Sequence 412, App
760	126.5	4.0	999	1	US-08-473-553A-5	Sequence 5, Appl	869	122	3.9	206	2	US-10-012-542-412	Sequence 412, App
761	126	4.0	143	2	US-08-893-737-190	Sequence 190, App	870	122	3.9	206	2	US-10-115-123-412	Sequence 412, App
762	126	4.0	152	2	US-09-270-767-33594	Sequence 33594, A	871	122	3.9	312	2	US-09-270-767-31750	Sequence 31750, A
763	126	4.0	775	2	US-09-949-016-8799	Sequence 8799, App	872	122	3.9	328	1	US-08-414-926A-9	Sequence 9, Appl
764	126	4.0	1485	2	US-09-762-569-4	Sequence 4, Appl	873	122	3.9	328	1	US-08-926-922-9	Sequence 9, Appl
785	125.5	4.0	440	2	US-08-985-335-3	Sequence 5338, App	874	122	3.9	328	2	US-09-253-682-9	Sequence 9, Appl
786	125.5	4.0	440	2	US-09-410-372-3	Sequence 3, Appl	875	122	3.9	328	2	US-09-527-657-9	Sequence 9, Appl
787	125.5	4.0	764	2	US-07-741-453A-54	Sequence 54, Appl	876	122	3.9	328	2	US-09-892-100-9	Sequence 9, Appl
788	125.5	4.0	764	2	US-07-741-453A-60	Sequence 60, Appl	877	122	3.9	481	2	US-09-949-016-9748	Sequence 9748, App
789	125.5	4.0	1129	2	US-09-023-905A-2	Sequence 2, Appl	878	122	3.9	495	2	US-09-352-991A-31949	Sequence 31949, A
790	125	4.0	419	2	US-10-002-344A-237	Sequence 237, App	879	122	3.9	515	2	US-09-252-991A-28127	Sequence 28127, A
791	125	4.0	757	2	US-09-252-991A-25918	Sequence 25918, A	880	122	3.9	527	2	US-09-370-838-216	Sequence 216, App
792	125	4.0	957	2	US-09-252-991A-20408	Sequence 20408, A	881	122	3.9	527	2	US-09-854-133-216	Sequence 216, App
793	125	4.0	1139	2	US-09-513-505-2	Sequence 2, Appl	882	122	3.9	529	2	US-09-716-964B-2	Sequence 2, Appl
794	125	4.0	2023	2	US-09-491-356C-8	Sequence 8, Appl	883	121.5	3.9	320	2	US-09-325-932A-190	Sequence 190, App
795	125	4.0	2026	2	US-09-487-558B-86	Sequence 86, Appl	884	121.5	3.9	344	2	US-10-094-749-2951	Sequence 2951, App
796	125	4.0	2124	2	US-09-538-092-1377	Sequence 1377, App	885	121.5	3.9	477	2	US-09-252-991A-19831	Sequence 19831, App
797	125	4.0	2294	2	US-09-252-991A-17231	Sequence 17231, App	886	121.5	3.9	695	2	US-09-248-796A-18020	Sequence 18020, A
798	124.5	4.0	107	2	US-09-270-767-61021	Sequence 61021, A	887	121.5	3.9	818	2	US-10-104-047-2546	Sequence 2546, App
799	124.5	4.0	283	2	US-10-211-689-4	Sequence 4, Appl	888	121.5	3.9	1225	2	US-09-501-171-4	Sequence 4, Appl
800	124.5	4.0	298	2	US-09-232-160-17	Sequence 17, Appl	889	121.5	3.9	1225	2	US-09-949-016-6063	Sequence 6063, App
801	124.5	4.0	298	2	US-09-800-729-87	Sequence 87, Appl	890	121.5	3.9	1251	5	PCT-US95-02251-3	Sequence 3, Appl
802	124.5	4.0	298	2	US-09-800-729-121	Sequence 121, App	891	121.5	3.9	1252	1	US-08-199-780-3	Sequence 3, Appl
803	124.5	4.0	298	2	US-10-000-489-22	Sequence 22, Appl	892	121.5	3.9	1252	1	US-08-316-650-3	Sequence 3, Appl
804	124.5	4.0	298	2	US-09-832-129-50	Sequence 50, Appl	893	121.5	3.9	1253	2	US-08-479-722B-4	Sequence 4, Appl
805	124.5	4.0	298	2	US-10-211-689-2	Sequence 2, Appl	894	121.5	3.9	1253	2	US-09-592-685-4	Sequence 4, Appl
806	124.5	4.0	298	2	US-09-992-095B-22	Sequence 22, Appl	895	121	3.9	499	2	US-09-049-672A-1	Sequence 1, Appl
807	124.5	4.0	298	3	US-10-000-986A-22	Sequence 22, App	896	121	3.9	739	2	US-09-902-540-10606	Sequence 10606, A
808	124.5	4.0	307	2	US-09-949-016-9817	Sequence 9817, App	897	121	3.9	910	2	US-09-228-986-72	Sequence 72, Appl
809	124.5	4.0	307	2	US-09-949-016-9818	Sequence 9818, App	898	121	3.9	910	2	US-10-101-464A-72	Sequence 72, Appl
820	124.5	4.0	307	2	US-09-949-016-9818	Sequence 9818, App	899	121	3.9	955	2	US-10-094-749-2652	Sequence 2652, App
827	124.5	4.0	623	2	US-09-949-016-6530	Sequence 6530, App	900	121	3.9	1139	2	US-09-513-505-4	Sequence 4, Appl
828	124.5	4.0	998	2	US-10-101-464A-895	Sequence 895, App	901	121	3.9	1742	3	US-09-958-359-23	Sequence 23, Appl
829	124.5	4.0	1042	2	US-09-252-991A-30444	Sequence 30444, A	902	120.5	3.8	54	2	US-09-973-424A-71	Sequence 71, Appl
830	124.5	4.0	1709	2	US-09-949-016-10503	Sequence 10503, A	903	120.5	3.8	141	1	US-08-442-063A-36	Sequence 36, Appl
831	124	4.0	277	2	US-07-741-453A-58	Sequence 58, Appl	904	120.5	3.8	426	2	US-09-252-991A-24450	Sequence 24450, A
832	124	4.0	707	2	US-09-228-986-80	Sequence 80, Appl	905	120.5	3.8	464	2	US-09-716-964B-4	Sequence 4, Appl
833	124	4.0	707	2	US-10-101-464A-80	Sequence 80, Appl	906	120.5	3.8	562	2	US-09-902-540-13269	Sequence 13269, A
834	124	4.0	1457	2	US-08-685-259-27	Sequence 27, Appl	907	120.5	3.8	787	2	US-09-721-383-2	Sequence 2, Appl
835	124	4.0	1457	2	US-08-762-500-27	Sequence 27, Appl	908	120.5	3.8	787	2	US-09-721-137-2	Sequence 2, Appl
836	124	4.0	1472	2	US-09-032-438C-119	Sequence 119, App	909	120.5	3.8	787	2	US-09-721-251-2	Sequence 2, Appl
837	123.5	3.9	1312	2	US-09-041-886-19	Sequence 19, Appl	910	120.5	3.8	787	2	US-10-114-764-2	Sequence 2, Appl
838	123.5	3.9	1312	2	US-09-648-281-2	Sequence 2, Appl	911	120.5	3.8	998	2	US-10-101-464A-931	Sequence 931, App
839	123.5	3.9	1312	2	US-09-707-919A-19	Sequence 19, Appl	912	120.5	3.8	1104	2	US-09-981-953A-4	Sequence 4, Appl
840	123.5	3.9	1312	2	US-08-083-268-3	Sequence 3, Appl	913	120.5	3.8	1587	2	US-09-949-002-354	Sequence 354, App
841	123.5	3.9	1312	2	US-08-981-998A-3	Sequence 3, Appl	914	120.5	3.8	1610	2	US-09-548-473B-4	Sequence 4, Appl
842	123	3.9	383	2	US-10-101-464A-898	Sequence 898, App	915	120.5	3.8	1665	2	US-09-858-664A-2	Sequence 2, Appl
843	123	3.9	526	2	US-09-252-991A-23688	Sequence 23688, App	916	120.5	3.8	1665	2	US-10-274-978-2	Sequence 2, Appl

917	120.5	3.8	1655	2	US-10-697-263-2	Sequence 2, Appli	990	117.5	3.7	1706	1	US-08-399-411-2	Sequence 2, Appli
918	120.5	3.8	2596	2	US-09-548-473B-6	Sequence 6, Appli	991	117.5	3.7	1706	2	US-08-516-859A-2	Sequence 2, Appli
919	120.5	3.8	2630	2	US-10-077-130-2	Sequence 2, Appli	992	117.5	3.7	1706	2	US-09-586-472-2	Sequence 2, Appli
920	120.5	3.8	7968	3	US-10-077-130-5	Sequence 5, Appli	993	117.5	3.7	1706	2	US-09-528-706-2	Sequence 2, Appli
921	120	3.8	130	2	US-09-270-767-33086	Sequence 33086, A	994	117.5	3.7	1706	2	US-10-024-450-2	Sequence 2, Appli
922	120	3.8	130	2	US-09-270-767-48303	Sequence 48303, A	995	117.5	3.7	1706	2	US-10-142-650-3	Sequence 3, Appli
923	120	3.8	467	2	US-09-046-736-2	Sequence 2, Appli	996	117	3.7	401	2	US-09-252-991A-32529	Sequence 32529, A
924	120	3.8	523	1	US-08-473-553A-3	Sequence 3, Appli	997	117	3.7	655	1	US-08-148-910-12	Sequence 12, Appl
925	120	3.8	569	2	US-09-514-245-22	Sequence 22, Appl	998	117	3.7	655	1	US-08-448-937A-12	Sequence 12, Appl
926	120	3.8	603	2	US-09-906-779-4	Sequence 4, Appli	999	117	3.7	809	2	US-09-252-991A-31759	Sequence 31759, A
927	120	3.8	696	2	US-09-758-759-125	Sequence 125, App	1000	117	3.7	888	2	US-09-252-991A-23787	Sequence 23787, A
928	120	3.8	710	2	US-10-094-749-2315	Sequence 2315, Ap	1001	117	3.7	980	1	US-08-473-553A-6	Sequence 6, Appli
929	120	3.8	2556	1	US-08-185-432-17	Sequence 17, Appl	1002	117	3.7	985	1	US-08-473-553A-2	Sequence 2, Appli
930	120	3.8	2556	2	US-08-899-232-2	Sequence 2, Appli	1003	117	3.7	1055	2	US-09-214-278-2	Sequence 2, Appli
931	120	3.8	2556	2	US-09-121-457-2	Sequence 2, Appli	1004	117	3.7	1055	2	US-09-855-722-2	Sequence 2, Appli
932	119.5	3.8	520	2	US-09-107-433-3721	Sequence 3721, Ap	1005	117	3.7	1148	2	US-08-882-046-4	Sequence 4, Appli
933	119.5	3.8	608	2	US-09-949-016-11148	Sequence 11148, A	1006	117	3.7	1148	2	US-09-566-047-4	Sequence 4, Appli
934	119.5	3.8	608	2	US-09-949-016-11149	Sequence 11149, A	1007	117	3.7	1193	1	US-08-400-159-10	Sequence 10, Appl
935	119.5	3.8	608	2	US-09-949-016-11150	Sequence 11150, A	1008	117	3.7	1193	2	US-08-611-729A-10	Sequence 10, Appl
936	119.5	3.8	608	2	US-09-949-016-11151	Sequence 11151, A	1009	117	3.7	1193	2	US-09-195-524-10	Sequence 10, Appl
937	119.5	3.8	1034	2	US-09-252-991A-28921	Sequence 28921, A	1010	117	3.7	1193	2	US-09-310-685-8	Sequence 8, Appli
938	119.5	3.8	1034	2	US-09-171-699-10	Sequence 10, Appl	1011	117	3.7	1212	2	US-09-214-278-3	Sequence 3, Appli
939	119.5	3.8	1149	2	US-08-560-005-5	Sequence 5, Appli	1012	117	3.7	1212	2	US-09-855-722-3	Sequence 3, Appli
940	119.5	3.8	1149	2	US-09-418-540-5	Sequence 5, Appli	1013	117	3.7	1238	2	US-09-214-278-5	Sequence 5, Appli
941	119.5	3.8	1149	2	US-09-869-528-5	Sequence 5, Appli	1014	117	3.7	1238	2	US-09-855-722-5	Sequence 5, Appli
942	119.5	3.8	1345	3	US-10-433-794-17	Sequence 17, Appl	1015	117	3.7	1237	2	US-08-611-729A-8	Sequence 8, Appli
943	119.5	3.8	1596	2	US-09-538-092-887	Sequence 887, App	1016	117	3.7	1237	2	US-09-195-524-8	Sequence 8, Appli
944	119	3.8	304	2	US-10-101-464A-717	Sequence 717, App	1017	117	3.7	1257	2	US-09-310-685-6	Sequence 6, Appli
945	119	3.8	319	2	US-08-630-172-12	Sequence 12, Appl	1018	117	3.7	2038	3	US-10-433-794-18	Sequence 18, Appl
946	119	3.8	319	2	US-09-375-419-12	Sequence 12, Appl	1019	116.5	3.7	132	2	US-10-101-464A-572	Sequence 572, App
947	119	3.8	528	2	US-08-328-213B-8	Sequence 8, Appli	1020	116.5	3.7	296	2	US-09-270-767-37880	Sequence 37880, A
948	119	3.8	593	2	US-09-252-991A-20441	Sequence 20441, A	1021	116.5	3.7	296	2	US-09-270-767-53197	Sequence 53197, A
949	119	3.8	784	2	US-09-982-308B-23	Sequence 23, Appl	1022	116.5	3.7	439	2	US-10-300-819B-21	Sequence 21, Appl
950	119	3.8	1081	2	US-09-369-364A-17	Sequence 17, Appl	1023	116.5	3.7	439	2	US-08-476-515A-12	Sequence 12, Appl
951	118.5	3.8	171	2	US-09-270-767-43049	Sequence 43049, A	1024	116.5	3.7	944	2	US-08-652-877-12	Sequence 12, Appl
952	118.5	3.8	422	2	US-09-949-016-8251	Sequence 8251, Ap	1025	116.5	3.7	1252	2	US-09-302-540-13967	Sequence 13967, A
953	118.5	3.8	430	2	US-09-949-016-8782	Sequence 8782, Ap	1026	116.5	3.7	2887	2	US-08-462-467B-8	Sequence 8, Appli
954	118.5	3.8	486	1	US-08-450-360-2	Sequence 2, Appli	1027	116.5	3.7	4854	2	US-08-476-515A-84	Sequence 84, Appl
955	118.5	3.8	883	2	US-10-188-495-72	Sequence 72, Appl	1028	116.5	3.7	4655	2	US-08-652-877-84	Sequence 84, Appl
956	118.5	3.8	1166	2	US-10-104-047-2949	Sequence 2949, Ap	1029	116.5	3.7	4655	2	US-08-652-877-86	Sequence 86, Appl
957	118.5	3.8	1321	1	US-08-317-310A-64	Sequence 64, Appl	1030	116.5	3.7	4655	2	US-08-652-877-88	Sequence 88, Appl
958	118	3.8	149	2	US-09-270-767-32618	Sequence 32618, A	1031	116.5	3.7	4655	2	US-08-652-877-90	Sequence 90, Appl
959	118	3.8	149	2	US-09-270-767-47835	Sequence 47835, A	1032	116	3.7	193	2	US-09-270-767-44942	Sequence 44942, A
960	118	3.8	462	2	US-09-252-991A-20814	Sequence 20814, A	1033	116	3.7	264	2	US-09-252-991A-24670	Sequence 24670, A
961	118	3.8	947	2	US-09-252-991A-21335	Sequence 21335, A	1034	116	3.7	383	2	US-10-094-749-2006	Sequence 2006, Ap
962	118	3.8	1044	2	US-09-252-991A-18853	Sequence 18853, A	1035	116	3.7	1053	2	US-09-513-505-8	Sequence 8, Appli
963	118	3.8	1064	2	US-09-252-991A-17508	Sequence 17508, A	1036	116	3.7	1181	2	US-09-826-509-587	Sequence 587, App
964	118	3.8	1084	2	US-09-227-725A-3	Sequence 3, Appli	1037	116	3.7	1291	2	US-09-150-460B-10	Sequence 10, Appl
965	118	3.8	1084	2	US-10-071-900-3	Sequence 3, Appli	1038	116	3.7	1291	2	US-09-220-641-5	Sequence 5, Appli
966	118	3.8	1864	1	US-08-804-227C-3	Sequence 3, Appli	1039	116	3.7	1351	2	US-09-548-473B-1	Sequence 1, Appli
967	118	3.8	2471	1	US-08-185-432-16	Sequence 16, Appl	1040	116	3.7	2556	1	US-08-083-590A-20	Sequence 20, Appl
968	118	3.8	2471	1	US-08-083-590A-19	Sequence 19, Appl	1041	116	3.7	2556	1	US-08-532-384-20	Sequence 20, Appl
969	118	3.8	2471	2	US-08-532-384-19	Sequence 19, Appl	1042	115.5	3.7	138	2	US-09-191-647-4	Sequence 4, Appli
970	118	3.8	2471	2	US-08-899-232-1	Sequence 1, Appli	1043	115.5	3.7	138	2	US-09-540-245A-4	Sequence 4, Appli
971	118	3.8	2471	2	US-09-121-457-1	Sequence 1, Appli	1044	115.5	3.7	138	2	US-09-540-153-4	Sequence 4, Appli
972	117.5	3.7	129	2	US-09-513-999C-4304	Sequence 4304, Ap	1045	115.5	3.7	138	2	US-10-289-776-4	Sequence 4, Appli
973	117.5	3.7	189	2	US-10-101-464A-517	Sequence 517, App	1046	115.5	3.7	412	2	US-09-252-991A-24484	Sequence 24484, A
974	117.5	3.7	190	1	US-08-441-629-4	Sequence 4, Appli	1047	115.5	3.7	728	2	US-09-252-991A-28169	Sequence 28169, A
975	117.5	3.7	190	2	US-08-776-207-4	Sequence 4, Appli	1048	115.5	3.7	1093	2	US-08-545-860B-55	Sequence 55, Appl
976	117.5	3.7	190	2	US-09-507-773-4	Sequence 4, Appli	1049	115.5	3.7	1093	2	PCT-US94-04496-55	Sequence 55, Appl
977	117.5	3.7	190	2	US-10-016-447-4	Sequence 4, Appli	1050	115	3.7	305	2	US-09-325-932A-188	Sequence 188, App
978	117.5	3.7	190	5	PCT-US95-09172-4	Sequence 4, Appli	1051	115	3.7	447	1	US-08-450-360-4	Sequence 4, Appli
979	117.5	3.7	247	2	US-10-101-464A-730	Sequence 730, App	1052	115	3.7	717	2	US-10-094-749-2120	Sequence 2120, Ap
980	117.5	3.7	563	2	US-09-252-991A-17549	Sequence 17549, A	1053	115	3.7	764	2	US-07-741-453A-59	Sequence 59, Appl
981	117.5	3.7	635	1	US-08-484-101B-36	Sequence 36, Appl	1054	115	3.7	764	2	US-07-741-453A-61	Sequence 61, Appl
982	117.5	3.7	635	1	US-08-484-101B-50	Sequence 50, Appl	1055	115	3.7	984	2	US-09-287-354-2	Sequence 2, Appli
983	117.5	3.7	635	2	US-08-714-524D-36	Sequence 36, Appl	1056	115	3.7	984	2	US-10-024-368-2	Sequence 2, Appli
984	117.5	3.7	635	2	US-08-714-524D-50	Sequence 50, Appl	1057	115	3.7	1053	2	US-09-513-505-6	Sequence 6, Appli
985	117.5	3.7	996	2	US-10-101-464A-889	Sequence 889, App	1058	115	3.7	1093	2	US-09-252-991A-21827	Sequence 21827, A
986	117.5	3.7	996	2	US-10-101-464A-933	Sequence 933, App	1059	115	3.7	1189	2	US-09-287-354-4	Sequence 4, Appli
987	117.5	3.7	1118	2	US-09-252-991A-24340	Sequence 24340, A	1060	115	3.7	1189	2	US-09-949-016-6931	Sequence 6931, Ap
988	117.5	3.7	1506	2	US-10-142-650-4	Sequence 4, Appli	1061	115	3.7	1189	2	US-10-024-368-4	Sequence 4, Appli
989	117.5	3.7	1706	1	US-08-459-568-2	Sequence 2, Appli	1062	115	3.7	1219	2	US-08-882-046-5	Sequence 5, Appli

1063	115	3.7	1219	2	US-09-566-047-5	Sequence 5, Appll	1136	113	3.6	1733	3	US-09-958-359-21	Sequence 21, Appl
1064	115	3.7	2415	2	US-09-949-002-398	Sequence 398, App	1137	112.5	3.6	328	2	US-09-252-991A-17729	Sequence 17729, A
1065	114.5	3.7	166	2	US-09-270-767-59438	Sequence 59438, A	1138	112.5	3.6	677	1	US-08-188-582-13	Sequence 13, Appl
1066	114.5	3.7	545	2	US-09-949-002-297	Sequence 297, App	1139	112.5	3.6	677	1	US-08-646-715-13	Sequence 13, Appl
1067	114.5	3.7	545	2	US-09-509-5958-2	Sequence 2, Appll	1140	112.5	3.6	677	2	US-09-538-092-1164	Sequence 1164, Ap
1068	114.5	3.7	545	2	US-09-509-5958-8	Sequence 8, Appll	1141	112.5	3.6	694	2	US-09-949-016-8774	Sequence 8774, Ap
1069	114.5	3.7	587	2	US-09-949-016-8708	Sequence 8708, Ap	1142	112.5	3.6	694	2	US-09-949-016-8775	Sequence 8775, Ap
1070	114.5	3.7	587	2	US-09-949-016-8709	Sequence 8709, Ap	1143	112.5	3.6	711	2	US-09-949-016-8493	Sequence 8493, Ap
1071	114.5	3.7	587	2	US-09-949-002-461	Sequence 461, App	1144	112.5	3.6	825	2	US-10-094-749-3083	Sequence 3083, Ap
1072	114.5	3.7	661	2	US-09-949-016-9121	Sequence 9121, Ap	1145	112.5	3.6	1068	1	US-08-396-479B-12	Sequence 12, Appl
1073	114.5	3.7	804	2	US-10-101-464A-890	Sequence 890, App	1146	112.5	3.6	1068	1	US-08-818-823-12	Sequence 12, Appl
1074	114.5	3.7	935	2	US-09-902-540-16200	Sequence 16200, A	1147	112.5	3.6	1078	2	US-09-949-016-9573	Sequence 9573, Ap
1075	114.5	3.7	1010	2	US-08-882-046-7	Sequence 7, Appll	1148	112	3.6	230	2	US-09-252-991A-31737	Sequence 31737, A
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1077	114.5	3.7	1017	2	US-09-600-776-6	Sequence 6, Appll	1150	112	3.6	241	2	US-08-470-335-195	Sequence 195, App
1078	114.5	3.7	1017	2	US-09-965-830-6	Sequence 6, Appll	1151	112	3.6	241	2	US-08-470-339-195	Sequence 195, App
1079	114.5	3.7	1036	2	US-09-068-740A-6	Sequence 6, Appll	1152	112	3.6	241	2	US-08-467-602-389	Sequence 389, App
1080	114.5	3.7	1067	2	US-09-579-536C-18	Sequence 18, Appl	1153	112	3.6	241	2	US-08-411-295F-47	Sequence 47, Appl
1081	114.5	3.7	1162	1	US-08-728-323A-2	Sequence 2, Appll	1154	112	3.6	241	2	US-08-411-295F-94	Sequence 94, Appl
1082	114.5	3.7	1162	2	US-09-298-568-2	Sequence 2, Appll	1155	112	3.6	297	1	US-08-580-545B-6	Sequence 6, Appll
1083	114.5	3.7	1162	2	US-09-410-399-2	Sequence 2, Appll	1156	112	3.6	297	2	US-09-262-653A-6	Sequence 6, Appll
1084	114.5	3.7	1162	2	US-09-894-273-2	Sequence 2, Appll	1157	112	3.6	383	1	US-08-597-545-2	Sequence 2, Appll
1085	114.5	3.7	1187	2	US-09-068-740A-7	Sequence 7, Appll	1158	112	3.6	383	1	US-08-457-135-2	Sequence 2, Appll
1086	114.5	3.7	1208	2	US-09-199-865-1	Sequence 1, Appll	1159	112	3.6	383	2	US-09-142-027A-12	Sequence 12, Appl
1087	114.5	3.7	1208	2	US-10-213-329-1	Sequence 1, Appll	1160	112	3.6	388	2	US-09-644-858-11	Sequence 11, Appl
1088	114.5	3.7	1218	1	US-08-400-159-6	Sequence 6, Appll	1161	112	3.6	404	2	US-10-094-749-3089	Sequence 3089, Ap
1089	114.5	3.7	1218	2	US-08-611-729A-6	Sequence 6, Appll	1162	112	3.6	417	2	US-09-644-858-5	Sequence 5, Appll
1090	114.5	3.7	1218	2	US-08-882-046-2	Sequence 2, Appll	1163	112	3.6	417	2	US-09-644-858-8	Sequence 8, Appll
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1092	114.5	3.7	1218	2	US-09-566-047-2	Sequence 2, Appll	1165	112	3.6	479	2	US-09-252-991A-23144	Sequence 23144, A
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1094	114.5	3.7	1218	2	US-09-195-524-6	Sequence 6, Appll	1167	112	3.6	513	1	US-08-659-235C-14	Sequence 14, Appl
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1097	114.5	3.7	1218	2	US-09-310-685-4	Sequence 4, Appll	1170	112	3.6	764	2	US-07-757-342B-5	Sequence 5, Appll
1098	114.5	3.7	1259	2	US-09-949-016-10297	Sequence 10297, A	1171	112	3.6	764	2	US-09-461-657B-5	Sequence 5, Appll
1099	114.5	3.7	2169	2	US-09-949-016-6930	Sequence 6930, Ap	1172	112	3.6	764	2	US-09-826-509-395	Sequence 395, App
1100	114	3.6	111	2	US-09-220-528-53	Sequence 53, Appl	1173	112	3.6	764	2	US-09-826-509-399	Sequence 399, App
1101	114	3.6	224	2	US-09-220-528-29	Sequence 29, Appl	1174	112	3.6	764	2	US-09-826-509-403	Sequence 403, App
1102	114	3.6	224	2	US-09-347-613C-16	Sequence 16, Appl	1175	112	3.6	764	2	US-09-826-509-407	Sequence 407, App
1103	114	3.6	224	2	US-09-662-183A-16	Sequence 16, Appl	1176	112	3.6	764	2	US-09-826-509-411	Sequence 411, App
1104	114	3.6	257	2	US-10-101-464A-743	Sequence 743, App	1177	112	3.6	764	2	US-09-826-509-415	Sequence 415, App
1105	114	3.6	497	2	US-10-104-047-3773	Sequence 3773, Ap	1178	112	3.6	764	2	US-09-826-509-419	Sequence 419, App
1106	114	3.6	631	2	US-09-270-767-44123	Sequence 44123, A	1179	112	3.6	764	2	US-09-826-509-423	Sequence 423, App
1107	114	3.6	644	1	US-08-866-757-2	Sequence 2, Appll	1180	112	3.6	902	1	US-08-396-479B-6	Sequence 6, Appll
1108	114	3.6	644	2	US-09-153-593-2	Sequence 2, Appll	1181	112	3.6	902	1	US-08-818-823-6	Sequence 6, Appll
1109	114	3.6	681	2	US-10-104-047-3586	Sequence 3586, Ap	1182	112	3.6	990	2	US-10-101-464A-814	Sequence 814, App
1110	114	3.6	875	2	US-09-150-460B-7	Sequence 7, Appll	1183	112	3.6	1833	2	US-08-479-722B-2	Sequence 2, Appll
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1112	114	3.6	1063	1	US-08-127-499A-8	Sequence 8, Appll	1185	112	3.6	1833	5	PCT-US95-02251-18	Sequence 18, Appl
1113	114	3.6	1063	1	US-08-482-847-8	Sequence 8, Appll	1186	111.5	3.6	228	2	US-09-902-540-15349	Sequence 15349, A
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1115	114	3.6	1290	2	US-09-150-460A-6	Sequence 6, Appll	1188	111.5	3.6	281	2	US-10-101-464A-619	Sequence 619, App
1116	114	3.6	3571	2	US-09-911-842A-2	Sequence 2, Appll	1189	111.5	3.6	320	2	US-09-252-991A-21056	Sequence 21056, A
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1120	113.5	3.6	246	2	US-09-973-424A-61	Sequence 61, Appl	1193	111.5	3.6	445	2	US-09-252-991A-22368	Sequence 22368, A
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1123	113.5	3.6	1164	2	US-09-902-540-12627	Sequence 12627, A	1196	111.5	3.6	841	2	US-09-949-016-9797	Sequence 9797, Ap
1124	113.5	3.6	1218	2	US-09-214-278-7	Sequence 7, Appll	1197	111.5	3.6	1021	2	US-10-101-464A-954	Sequence 954, App
1125	113.5	3.6	1218	2	US-09-855-722-7	Sequence 7, Appll	1198	111.5	3.6	1298	1	US-08-690-473-2	Sequence 2, Appll
1126	113	3.6	175	2	US-10-101-464A-801	Sequence 801, App	1199	111.5	3.6	1298	2	US-09-259-821A-2	Sequence 2, Appll
1127	113	3.6	369	2	US-09-252-991A-25394	Sequence 25394, A	1200	111.5	3.6	1298	2	US-08-843-659-2	Sequence 2, Appll
1128	113	3.6	681	2	US-10-362-247-2	Sequence 2, Appll	1201	111.5	3.6	1298	2	US-09-825-288A-2	Sequence 2, Appll
1129	113	3.6	688	2	US-09-367-206-20	Sequence 20, Appl	1202	111	3.5	269	2	US-09-252-991A-21250	Sequence 21250, A
1130	113	3.6	688	2	US-09-298-404-20	Sequence 20, Appl	1203	111	3.5	267	2	US-08-818-112-142	Sequence 142, App
1131	113	3.6	723	2	US-10-104-047-2246	Sequence 2246, Ap	1204	111	3.5	267	2	US-08-818-111-137	Sequence 137, App
1132	113	3.6	770	2	US-09-981-953A-2	Sequence 2, Appll	1205	111	3.5	267	2	US-09-056-556-142	Sequence 142, App
1133	113	3.6	979	2	US-09-538-092-990	Sequence 990, App	1206	111	3.5	267	2	US-09-072-596-137	Sequence 137, App
1134	113	3.6	1247	2	US-09-501-171-6	Sequence 6, Appll	1207	111	3.5	267	2	US-09-072-567-142	Sequence 142, App
1135	113	3.6	1717	3	US-09-958-359-20	Sequence 20, Appl	1208	111	3.5	267	2	US-10-193-002-137	Sequence 137, App

1209	111	3.5	267	2	US-10-084-843-142	Sequence 142, App	1282	109.5	3.5	343	2	US-10-101-464A-892	Sequence 892, App
1210	111	3.5	332	2	US-09-252-991A-29259	Sequence 29259, A	1283	109.5	3.5	381	2	US-10-101-464A-660	Sequence 660, App
1211	111	3.5	333	2	US-09-252-991A-19956	Sequence 19956, A	1284	109.5	3.5	400	2	US-10-101-464A-939	Sequence 939, App
1212	111	3.5	452	2	US-09-949-016-7289	Sequence 7289, Ap	1285	109.5	3.5	401	7	5252556-1	Patent No. 5252556
1213	111	3.5	454	2	US-09-716-9648-5	Sequence 5, Appli	1286	109.5	3.5	456	2	US-08-470-335-246	Sequence 246, App
1214	111	3.5	492	1	US-08-644-271-32	Sequence 32, Appl	1287	109.5	3.5	456	2	US-08-467-602-303	Sequence 303, App
1215	111	3.5	492	1	US-09-077-955-36	Sequence 36, Appl	1288	109.5	3.5	456	2	US-08-411-2958-229	Sequence 229, App
1216	111	3.5	492	2	US-10-016-283-36	Sequence 36, Appl	1289	109.5	3.5	490	2	US-08-467-602-345	Sequence 345, App
1217	111	3.5	595	2	US-09-949-016-7205	Sequence 7205, Ap	1290	109.5	3.5	490	2	US-08-411-2958-271	Sequence 271, App
1218	111	3.5	699	2	US-07-757-3420-2	Sequence 2, Appli	1291	109.5	3.5	612	1	US-08-359-705B-8	Sequence 8, Appli
1219	111	3.5	699	2	US-09-461-6578-2	Sequence 2, Appli	1292	109.5	3.5	612	1	US-08-286-846A-8	Sequence 8, Appli
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1221	111	3.5	1109	2	US-09-949-016-10771	Sequence 10771, A	1294	109.5	3.5	612	2	US-08-444-622A-8	Sequence 8, Appli
1222	111	3.5	1203	2	US-09-949-016-6615	Sequence 6615, Ap	1295	109.5	3.5	612	2	US-08-942-562-8	Sequence 8, Appli
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1224	111	3.5	1318	2	US-10-237-551-197	Sequence 197, App	1297	109.5	3.5	632	2	US-09-252-991A-25544	Sequence 25544, A
1225	111	3.5	1358	1	US-08-404-665-4	Sequence 4, Appli	1298	109.5	3.5	690	2	US-09-228-986-69	Sequence 69, Appl
1226	111	3.5	1358	1	US-08-404-671-4	Sequence 4, Appli	1299	109.5	3.5	690	2	US-10-101-464A-69	Sequence 69, Appl
1227	111	3.5	1358	1	US-08-404-781-4	Sequence 4, Appli	1300	109.5	3.5	690	2	US-09-949-016-7806	Sequence 7806, Ap
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1231	111	3.5	1650	2	US-09-252-991A-21798	Sequence 21798, A	1304	109.5	3.5	839	1	US-08-359-705B-8	Sequence 8, Appli
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1234	111	3.5	1719	2	US-08-516-859A-4	Sequence 4, Appli	1307	109.5	3.5	839	2	US-08-444-622A-6	Sequence 6, Appli
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1237	111	3.5	1719	2	US-10-024-450-4	Sequence 4, Appli	1310	109.5	3.5	904	2	US-09-252-991A-25286	Sequence 25286, A
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1239	111	3.5	2254	2	US-09-949-016-9270	Sequence 9270, Ap	1312	109.5	3.5	1235	2	US-09-949-016-8456	Sequence 8456, Ap
1240	111	3.5	2442	2	US-09-514-247A-10	Sequence 10, Appl	1313	109	3.5	163	2	US-09-252-991A-28374	Sequence 28374, A
1241	111	3.5	2442	2	US-09-538-092-1370	Sequence 1370, Ap	1314	109	3.5	221	1	US-08-480-229C-29	Sequence 29, Appl
1242	111	3.5	2523	1	US-08-185-432-18	Sequence 18, Appl	1315	109	3.5	221	1	US-08-659-235C-29	Sequence 29, Appl
1243	111	3.5	2523	2	US-08-899-232-3	Sequence 3, Appli	1316	109	3.5	259	2	US-10-094-749-2303	Sequence 2303, Ap
1244	111	3.5	2523	2	US-09-121-457-3	Sequence 3, Appli	1317	109	3.5	416	2	US-08-978-289-12	Sequence 12, Appl
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ALIGNMENTS

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RESULT 1
; Sequence 69, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien

Query Match      100.0%; Score 3135; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. NO. 7.3e-217;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Patent No. 6734288
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; APPLICANT: Baker, Kevin
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; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
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; APPLICANT: Godowski, Paul
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; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,457
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
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; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6734288ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6734288ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-457-69

Query Match      100.0%; Score 3135; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 7.3e-217;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MCSRVPLLLPLLLALGPGVQCSCQCSQPTVFCTARQGTTPRDPVPPDTVGLYVF 60
Db      1 MCSRVPLLLPLLLALGPGVQCSCQCSQPTVFCTARQGTTPRDPVPPDTVGLYVF 60

Qy      61 ENGITMLDASSFAGLPGQLLDLSONQIASRLRLRLLLDLSHNSLLALEPGILDTANVE 120
Db      61 ENGITMLDASSFAGLPGQLLDLSONQIASRLRLRLLLDLSHNSLLALEPGILDTANVE 120

Qy      121 ALRLAGLQQLDGLSRLNHLHDLDVSDNQLSERVPPVIRGLRGLRLRGLAGNTRIAQL 180
Db      121 ALRLAGLQQLDGLSRLNHLHDLDVSDNQLSERVPPVIRGLRGLRLRGLAGNTRIAQL 180

Qy      181 RPELAGLAAQLDGLSRLNHLHDLDVSDNQLSERVPPVIRGLRGLRLRGLAGNTRIAQL 240
Db      181 RPELAGLAAQLDGLSRLNHLHDLDVSDNQLSERVPPVIRGLRGLRLRGLAGNTRIAQL 240

Qy      241 SHVTLASPEETRCHFFPKNAGRLLELDYADFGCPATTATVPTTRPVVREPTALSSSL 300
Db      241 SHVTLASPEETRCHFFPKNAGRLLELDYADFGCPATTATVPTTRPVVREPTALSSSL 300

Qy      301 APTWLSPTAPATEAPSPSTAPPTVGPVPPQDCPPSTCLNGGTCHLGRHHLACLCPG 360
Db      301 APTWLSPTAPATEAPSPSTAPPTVGPVPPQDCPPSTCLNGGTCHLGRHHLACLCPG 360

; 361 FTGLYCESQMGQGTTRPSPPTVTPRPRSLTLGIEPVSPSTSLRVLGRLYLOGSSVQLRSR 420
; 361 FTGLYCESQMGQGTTRPSPPTVTPRPRSLTLGIEPVSPSTSLRVLGRLYLOGSSVQLRSR 420
; 421 LTVRNLSGPDKRLVTLRLPASLAETVTLQLRPNATYSVCVMPPLGPGRVPEGEACGEAHT 480
; 421 LTVRNLSGPDKRLVTLRLPASLAETVTLQLRPNATYSVCVMPPLGPGRVPEGEACGEAHT 480
; 481 PPAVHSHNAPVTVQAREGNLPLLIAPALAAVLLAALAAGAAVAVVRRGRAMAAAAQDKGV 540
; 481 PPAVHSHNAPVTVQAREGNLPLLIAPALAAVLLAALAAGAAVAVVRRGRAMAAAAQDKGV 540
; 541 GPAGGLEGVKVPLEPGPKATGEGGEGALPGSSECEVPLMGFPGLQSLPHAKPYI 598
; 541 GPAGGLEGVKVPLEPGPKATGEGGEGALPGSSECEVPLMGFPGLQSLPHAKPYI 598

RESULT 3
; Sequence 69, Application US/09945584
; Patent No. 6908993
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,584
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
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; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6908993ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6908993ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien

Query Match 100.0%; Score 3135; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 7.3e-217; Mismatches 0; Indels 0; Gaps 0;
Matches 598; Conservative 0;

Qy 1 MCSRVPLLLPLLLALLGPGVQCQSCQSQPQVCTARQGTTPRDPVPPDVTGLYVF 60
Db 1 MCSRVPLLLPLLLALLGPGVQCQSCQSQPQVCTARQGTTPRDPVPPDVTGLYVF 60

Qy 61 ENGITMLDASSFAGLPGQLLDLSQNOIASLRLPRLLLDLSHNSLLALEPGLDITANVE 120
Db 61 ENGITMLDASSFAGLPGQLLDLSQNOIASLRLPRLLLDLSHNSLLALEPGLDITANVE 120

Qy 121 ALRLAGLGLQDLDEGLFSRLNHLHDVSDNQLRVPVIRGLRGLRTRLAGNTRIAQL 180
Db 121 ALRLAGLGLQDLDEGLFSRLNHLHDVSDNQLRVPVIRGLRGLRTRLAGNTRIAQL 180

Qy 181 RPEDLAGLALQELDVNSLSIALPGDLISGLFPRLRLLLAARNPFCVCLSWFPGPVRE 240
Db 181 RPEDLAGLALQELDVNSLSIALPGDLISGLFPRLRLLLAARNPFCVCLSWFPGPVRE 240

Qy 241 SHVTLASPEETRCHFFPKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
Db 241 SHVTLASPEETRCHFFPKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300

; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
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; PRIOR FILING DATE: March 3, 1999
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; PRIOR FILING DATE: No. 6908993ember 30, 1999
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; PRIOR FILING DATE: February 11, 2000
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; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien

; Sequence 69, Application US/09944944
; Patent No. 6929947
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavina, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,944
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
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[illegible]

Db	1	MCSRVPPLLLPLLLLLALPGVQGCPCGCQSQQTFTARQGTTPRDVPPDVTGLVVF	60
Qy	61	ENGITMLDASSFAGLPGQLLDLSONQIASIRLRLLLDLSHNSLLALEPGILDTANVE	120
Db	61	ENGITMLDASSFAGLPGQLLDLSONQIASIRLRLLLDLSHNSLLALEPGILDTANVE	120
Qy	121	ALRLAGLQQLQDEGLFSRLNLHDLVDSONQLERVPVIRGLRGLTRLAGNTRIAQL	180
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Db	181	RPEDLAGLAALQELDVNSLSQALPGDLGSLFPRLRLAAARNPFCVCLSWFGPWVRE	240
Qy	241	SHVTLASPEETRCHFPKNAAGRLLELDYADFGCPATTTATVTPRPVREPTALSSSL	300
Db	241	SHVTLASPEETRCHFPKNAAGRLLELDYADFGCPATTTATVTPRPVREPTALSSSL	300
Qy	301	APTWLSPTAPATEAPSPPTAPPTVGPVPOQDCPPSTCLNGGTCHLGRHLACLCEG	360
Db	301	APTWLSPTAPATEAPSPPTAPPTVGPVPOQDCPPSTCLNGGTCHLGRHLACLCEG	360
Qy	361	FTGLYCQSQGQGRPSPTPTPRPRSLTLGIEPVSPSTSLRVGLQRYLQSSVQLRSLR	420
Db	361	FTGLYCQSQGQGRPSPTPTPRPRSLTLGIEPVSPSTSLRVGLQRYLQSSVQLRSLR	420
Qy	421	LYRNLSGPKRLVTLRLPASLAETVTLQRPNATYSVCVMPGLGPRVPEGEACGEAHT	480
Db	421	LYRNLSGPKRLVTLRLPASLAETVTLQRPNATYSVCVMPGLGPRVPEGEACGEAHT	480
Qy	481	PPAVHSHNAPVTOAREGNLPLLIAPALAAVLAALAAVGAAYCVRGRAMAAAAQDKGV	540
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Qy	541	GPAGAPLEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGLQSPHLAKPYI	598
Db	541	GPAGAPLEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGLQSPHLAKPYI	598

RESULT 7
US-09-063-950-2
; Sequence 2, Application US/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MBI-019
; CURRENT APPLICATION NUMBER: US/09/063,950C
; CURRENT FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in ver. 2.0
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-063-950-2

Query Match 98.4%; Score 3083.5; DB 2; Length 673;
Best Local Similarity 88.7%; Pred. No. 4.2e-213;
Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

Qy	1	MCSRVPPLLLPLLLLLALPGVQGCPCGCQSQQTFTARQGTTPRDVPPDVTGLVVF	60
Db	1	MCSRVPPLLLPLLLLLALPGVQGCPCGCQSQQTFTARQGTTPRDVPPDVTGLVVF	60
Qy	61	ENGITMLDASSFAGLPGQLLDLSONQIASIRLRLLLDLSHNSLLALEPGILDTANVE	120
Db	61	ENGITMLDASSFAGLPGQLLDLSONQIASIRLRLLLDLSHNSLLALEPGILDTANVE	120
Qy	91	-----LRLPRLLLDLSHNS	105

Db	121	RGURRLERLYLGNRRIRHIQPGAFDTLDRLLLEKLQDNELRALPPLRLPRLLLDLSHNS	180
Qy	106	LLALEPGIILDTANVEALRLAGLQQLQDEGLFSRLNLHDLVDSONQLERVPVIRGLRG	165
Db	181	LLALEPGIILDTANVEALRLAGLQQLQDEGLFSRLNLHDLVDSONQLERVPVIRGLRG	240
Qy	166	LTRLRAGNTRIAQLRPEDLAGLAALQELDVNSLSQALPGDLGSLFPRLRLAAARNPF	225
Db	241	LTRLRAGNTRIAQLRPEDLAGLAALQELDVNSLSQALPGDLGSLFPRLRLAAARNPF	300
Qy	226	NCVCPLSWFGPWVRESHVTLASPEETRCHFPKNAAGRLLELDYADFGCPATTTATVPT	285
Db	301	NCVCPLSWFGPWVRESHVTLASPEETRCHFPKNAAGRLLELDYADFGCPATTTATVPT	360
Qy	286	TRPVREPTALSSSLAPTMLSPTAPATEAPSPPTAPPTVGPVPOQDCPPSTCLNGGTC	345
Db	361	TRPVREPTALSSSLAPTMLSPTAPATEAPSPPTAPPTVGPVPOQDCPPSTCLNGGTC	420
Qy	346	HLGTRHHLACLCEGFTGLYCQSQGQGRPSPTPTPRPRSLTLGIEPVSPSTSLRVGL	405
Db	421	HLGTRHHLACLCEGFTGLYCQSQGQGRPSPTPTPRPRSLTLGIEPVSPSTSLRVGL	480
Qy	406	QRYLQSSVQLRSLRVTYRNLSGPKRLVTLRLPASLAETVTLQRPNATYSVCVMPGLG	465
Db	481	QRYLQSSVQLRSLRVTYRNLSGPKRLVTLRLPASLAETVTLQRPNATYSVCVMPGLG	540
Qy	466	GRVPEGEACGEAHTPPAVHSHNAPVTOAREGNLPLLIAPALAAVLAALAAVGAAYCVR	525
Db	541	GRVPEGEACGEAHTPPAVHSHNAPVTOAREGNLPLLIAPALAAVLAALAAVGAAYCVR	600
Qy	526	RGRAMAAAAQDKGVQGFAGAPLEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFP	585
Db	601	RGRAMAAAAQDKGVQGFAGAPLEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFP	660
Qy	586	PGLQSPHLAKPYI	598
Db	661	PGLQSPHLAKPYI	673

RESULT 8
; Sequence 52, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C53
; CURRENT APPLICATION NUMBER: US/09/991,181
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787

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Db	106	LLALEP	ILDTAN	VEAL	RLAG
	181	LLALEP	ILDTAN	VEAL	RLAG
Qy	166	LTRL	LAGN	TRIA	QIAR
	241	LTRL	LAGN	TRIA	QIAR
Db	226	NCVC	PLSW	FGPW	VRSH
	301	NCVC	PLSW	FGPW	VRSH
Qy	286	TRPV	REPT	ALSS	SLAP
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Db	345	HLGR	THHL	ACLP	CGFT
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Qy	406	QRYL	QSSV	QLRS	URLT
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Db	525	GRVE	PEGE	ACCE	ANTP
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Db	598	PGLQ	SPLH	AKPY	I 598
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RESULT 9

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
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; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444
; PRIOR FILING DATE: 2001-11-14
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;; PRIOR FILING DATE: 1998-07-09

Query Match 98.4%; Score 3083.5; DB 2; Length 673;

Best Local Similarity 88.7%; Pred. No. 4-2e-213;
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Db 61 ENGITMLDAGSFAGLPGQLQLDLDSQNIASLPSGVFPQLANLNLDTANRLHEITNETF 120

Qy 91 -----LRLPRLLLDLSHNS 105

Db 121 RGLRRLRLYLGKNRIRHQPFGAFTDLRLLELKLQDNELRALPPLRLPRLLLDLSHNS 180

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Dd 301 NCVCPLSWFGPWVRESHVTLASPEETRCHPPKKNAGRLLELDYADFGCATTATTVPT 360
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RESULT 10
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; GENERAL INFORMATION:
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; APPLICANT: Tumas, Daniel
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C27
; CURRENT APPLICATION NUMBER: US/09/997,333
; CURRENT FILING DATE: 2001-11-15
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 98.4%; Score 3083.5; DB 2; Length 673;
Best Local Similarity 88.7%; Pred. No. 4.2e-213;
Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

Qy 1 MCSRVPLLLPLLLLLALGFGVQCPSGCCSQSQPQTVFCTARQGTTPRDPVPPDTVGLYVF 60
Db 1 MCSRVPLLLPLLLLLALGFGVQCPSGCCSQSQPQTVFCTARQGTTPRDPVPPDTVGLYVF 60
Qy 61 ENGITWLDASSPAGLPGLQLDLSQNCIAS----- 90
Db 61 ENGITWLDAGSFAGLPGLQLDLSQNCIAS-----LRLPRLLLLDLSHNS 120
Qy 91 -----LRLPRLLLLDLSHNS 105
Db 121 RGLRRLRLYLGKNRIRHIQPGAFDLDRLLEKLQDNELRALPRLRLPRLLLDLSHNS 180
Qy 106 LLALEFGILDNTANVEALRLAGLQQLDEGLFSLRLNHLHDLDVSDNQLERVPVIRGLRG 165
Db 181 LLALEFGILDNTANVEALRLAGLQQLDEGLFSLRLNHLHDLDVSDNQLERVPVIRGLRG 240
Qy 166 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSIQALPGDLSGLFPRLRLAARNPFF 225
Db 241 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSIQALPGDLSGLFPRLRLAARNPFF 300
Qy 226 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKPNAGRLLELDYADFPCPATTTATVPT 285
Db 301 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKPNAGRLLELDYADFPCPATTTATVPT 360
Qy 286 TRPVVREPTALSSSLAPTTLSPATAPATEAPSPSTAPPTVGPVPQDCCPPSTCLNGGTC 345
Db 361 TRPVVREPTALSSSLAPTTLSPATAPATEAPSPSTAPPTVGPVPQDCCPPSTCLNGGTC 420
Qy 346 HLGTRHHLACLCPGEGTGLYCESQMGQTRPSPTVTPRPPRSLTLGI EPVVSLSRVGL 405
Db 421 HLGTRHHLACLCPGEGTGLYCESQMGQTRPSPTVTPRPPRSLTLGI EPVVSLSRVGL 480
Qy 406 QRYLQSSSVQLRSLRLTYRNLSPDKRLVTLRPLASLAETVTLQLRPNATYSVCVWPLGP 465
Db 481 QRYLQSSSVQLRSLRLTYRNLSPDKRLVTLRPLASLAETVTLQLRPNATYSVCVWPLGP 540
Qy 466 GRVPEGEACGEAHTPPAVHSNHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 525
Db 541 GRVPEGEACGEAHTPPAVHSNHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 600
Qy 526 RGRMAAAADKGVGCPGAGPLEGKVPKATEGGEALPSGSECEVPLMGFP 585
Db 601 RGRMAAAADKGVGCPGAGPLEGKVPKATEGGEALPSGSECEVPLMGFP 660
Qy 586 PGLQSPHLHAKPYI 598
Db 661 PGLQSPHLHAKPYI 673

RESULT 11
; Sequence 52, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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Qy	106	LALALEPGILDTANVEALRLAGLGLOQLDEGLFSRLRNHLHDVDSDNQLERVPPVIRGLRG	165
Dd	181	LALALEPGILDTANVEALRLAGLGLOQLDEGLFSRLRNHLHDVDSDNQLERVPPVIRGLRG	240
Qy	166	LTRLRLAGNTRIAOLRPEDLAGLAALQELDVSNISLQNALPDGLSGLFPRLFLAAARNPF	225
Dd	241	LTRLRLAGNTRIAOLRPEDLAGLAALQELDVSNISLQNALPDGLSGLFPRLFLAAARNPF	300
Qy	226	NCVCPLSNWFGPWVRSHVHTLASPEETRCHPPPKNAGRLLLLEDVADFCGPATTTTATVPT	285
Dd	301	NCVCPLSNWFGPWVRSHVHTLASPEETRCHPPPKNAGRLLLLEDVADFCGPATTTTATVPT	360
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Qy	346	HGTRHHLACLCPGFTGLYCESQMGQTRSPTPTVTPRPRSITLGTIEPVSPTSRLRVGL	405
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Qy	406	QRYLQGSVVQLRSRLTRYNLSGDPKRLVTURLPASLAEYTVTQLRPNATTYSVCVMPLGP	465
Dd	481	QRYLQGSVVQLRSRLTRYNLSGDPKRLVTURLPASLAEYTVTQLRPNATTYSVCVMPLGP	540
Qy	466	GRVPEGBEACGEAHTPPAVHSNHAPVTOAREGNIPLIITAPALAAVLLAALAAGVAAYCVR	525
Dd	541	GRVPEGBEACGEAHTPPAVHSNHAPVTOAREGNIPLIITAPALAAVLLAALAAGVAAYCVR	600
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, PRIOR APPLICATION NUMBER: 60/091982
, PRIOR FILING DATE: 1998-07-07
, PRIOR APPLICATION NUMBER: 60/092182
, PRIOR FILING DATE: 1998-07-09

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	Query Match	98.4%	Score 3083.5	DB 3	Length 673
	Best Local Similarity	88.7%	Pred. No. 4.2e-213		
	Matches 597	Conservative 0	Mismatches 1	Indels 75	Gaps 1
Qy	1	MCSRVPLLLPLLLLLALGPGVQCQSPGSCQSQQTVECTARQGTTPRDVPPDVTGLVYVF	60		
Db	1	MCSRVPLLLPLLLLLALGPGVQCQSPGSCQSQQTVECTARQGTTPRDVPPDVTGLVYVF	60		
Qy	61	ENGITMLDASSFAGLPGQLQLDLSQNIAS-----	90		
Db	61	ENGITMLDAGSFAGLPGQLQLDLSQNIASLPSGVFQPLANSLDLTANRLHEITNETF	120		
Qy	91	-----	105		
Db	121	RGRLRLRYLGNKRIRHHPGAFDTRLRLLEKLQDNEURLAUPPLRLPRLLLDLSHNS	180		
Qy	106	LLALEPGILDANVEALRIAGLGIQQLDEGLFSRLRNRLHLDVSDNQLERVPVPIRLRG	165		

Db 181 LLALEPGILDTANVEARLRLAGLQDDEGLFSRLNHLDDVSDNQLRVPVIRLGR 240
Qy 166 LTRLRLAGNTRIAQRLPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRRLRLAAARNPF 225
Db 241 LTRLRLAGNTRIAQRLPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRRLRLAAARNPF 300
Qy 226 NCVCPLSWFGPWRESHVHTLASPBETRCHFPKPNAGRLLELDYADFGCPATTTATVPT 285
Db 301 NCVCPLSWFGPWRESHVHTLASPBETRCHFPKPNAGRLLELDYADFGCPATTTATVPT 360
Qy 286 TRPVREPTALSSSLATPWLSPATAPAEAPSPSTAPPTVGPVPODCCPPSCLNGGTC 345
Db 361 TRPVREPTALSSSLATPWLSPATAPAEAPSPSTAPPTVGPVPODCCPPSCLNGGTC 420
Qy 346 HLGRHRLHCLCPGFGTGLYCESQMGQGTSPSPFPVTPRPRSLTLGIEVPSPTSLRVLG 405
Db 421 HLGRHRLHCLCPGFGTGLYCESQMGQGTSPSPFPVTPRPRSLTLGIEVPSPTSLRVLG 480
Qy 406 QRYLQSSVOLRSRLTYRNLSGDPKRLVTLRLPASLAETVTVTLRPNATYSVCMPLGP 465
Db 481 QRYLQSSVOLRSRLTYRNLSGDPKRLVTLRLPASLAETVTVTLRPNATYSVCMPLGP 540
Qy 466 GRVPEGEACGEAHTPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAAALAAAYCVR 525
Db 541 GRVPEGEACGEAHTPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAAALAAAYCVR 600
Qy 526 RGRAMAAADKQGVGAGFLEGVKVPLEPGPKATEGGEGALPSGSECEVPLMGFP 585
Db 601 RGRAMAAADKQGVGAGFLEGVKVPLEPGPKATEGGEGALPSGSECEVPLMGFP 660
Qy 586 PGLQSPHLAKPYI 598
Db 661 PGLQSPHLAKPYI 673

RESULT 14

Sequence 52, Application US/09997514
Patent No. 7019116
GENERAL INFORMATION:
APPLICANT: Askenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC46
CURRENT APPLICATION NUMBER: US/09/997,514
CURRENT FILING DATE: 2001-11-15
PRIORITY FILING DATE: 2001-11-15
PRIORITY FILING DATE: 1997-06-16
PRIORITY FILING DATE: 1997-06-16
PRIORITY FILING DATE: 1997-10-17

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Sequence 52, Application US/09989728
Patent No. 7029873
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC72
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CURRENT FILING DATE: 2001-11-20
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GenCore version 6.2
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OM protein - protein search, using sw model

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(without alignments)
1457.908 Million cell updates/sec

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Post-processing: Minimum Match 0%
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Listing first 1500 summaries

Database : Published Applications AA.Main.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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379	360.5	11.5	635	5	US-10-363-374-8	Sequence 8, Appl
380	360.5	11.5	647	4	US-10-093-463-188	Sequence 188, App
381	357.5	11.4	778	4	US-10-093-463-192	Sequence 192, App
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384	337	10.7	653	3	US-09-957-187-10	Sequence 10, Appl
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917	329.5	10.5	775	4	US-11-290-153-438	Sequence 438, App
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8	2935	93.6	672	6	US-10-664-356-1475
9	2935	93.6	672	7	US-11-366-486-817
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18	316.5	10.1	713	7	US-11-030-653-26
19	313.5	10.0	656	7	US-11-030-653-38
20	312	10.0	592	6	US-10-486-020-19
21	312	10.0	592	7	US-11-030-653-14
24	309	9.9	649	7	US-11-101-316-132
25	309	9.9	649	7	US-11-376-673-132
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122	209	6.7	1091	6	US-10-219-051B-5403	Sequence 5403, Ap	203	175.5	5.6	492	6	US-10-537-102-14	Sequence 14, Appl
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126	206	6.6	428	6	US-10-405-027-5521	Sequence 5521, Ap	207	175	5.6	591	7	US-11-511-141-2	Sequence 2, Appli
127	206	6.6	428	6	US-10-405-027-5523	Sequence 5523, Ap	208	174	5.6	951	6	US-10-219-051B-921	Sequence 921, App
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138	200.5	6.4	295	6	US-11-366-486-654	Sequence 654, App	220	171.5	5.5	558	6	US-10-533-519-1564	Sequence 1564, Ap
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143	197.5	6.3	256	6	US-10-405-027-3896	Sequence 3896, Ap	225	170	5.4	907	7	US-10-219-051B-5044	Sequence 5044, Ap
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147	195	6.2	837	7	US-11-371-354-66139	Sequence 66139, A	229	168.5	5.4	907	7	US-11-486-332-11	Sequence 11, Appl
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178	182.5	5.7	290	7	US-11-257-579-12	Sequence 12, Appl	260	164	5.2	703	7	US-11-291-140-4	Sequence 4, Appli
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183	182.5	5.7	522	7	US-11-166-372-2689	Sequence 2689, Ap	265	164	5.2	904	7	US-10-540-808-2	Sequence 2, Appli
184	182.5	5.7	1043	7	US-11-387-182-2	Sequence 2, Appli	266	164	5.2	915	6	US-10-540-808-3	Sequence 3, Appli
185	182.5	5.7	1049	6	US-10-528-260B-205	Sequence 205, App	267	164	5.2	967	7	US-11-500-008-11	Sequence 11, Appl
186	182.5	5.7	1049	6	US-11-368-333-24	Sequence 24, Appl	268	164	5.2	2000	6	US-10-533-519-1676	Sequence 1676, Ap
187	182.5	5.7	1049	7	US-11-368-334-18	Sequence 18, Appl	269	164	5.2	2026	6	US-10-505-928-831	Sequence 831, App
188	182.5	5.7	1049	7	US-11-387-182-4	Sequence 4, Appli	270	164	5.2	639	7	US-11-056-355B-69825	Sequence 69825, A
189	182.5	5.7	1050	7	US-11-368-333-26	Sequence 26, Appl	271	163.5	5.2				
190	182.5	5.7	1050	7	US-11-368-334-22	Sequence 22, Appl							

272	163.5	5.2	674	7	US-11-056-3558-69824	Sequence 69824, A	348	154.5	4.9	854	7	US-11-389-343-1107	Sequence 1107, Ap
273	163.5	5.2	674	7	US-11-056-3558-75179	Sequence 75179, A	349	154.5	4.9	854	7	US-11-389-017-1098	Sequence 1098, Ap
274	163.5	5.2	765	7	US-11-056-3558-75178	Sequence 75178, A	350	154.5	4.9	854	7	US-11-389-017-1101	Sequence 1101, Ap
275	163.5	5.2	765	7	US-11-056-3558-69823	Sequence 69823, A	351	154.5	4.9	854	7	US-11-389-017-1103	Sequence 1103, Ap
276	163.5	5.2	826	7	US-11-056-3558-75177	Sequence 75177, A	352	154.5	4.9	854	7	US-11-389-017-1105	Sequence 1105, Ap
277	163	5.2	826	7	US-11-056-3558-75177	Sequence 75177, A	353	154.5	4.9	854	7	US-11-389-017-1107	Sequence 1107, Ap
278	163	5.2	753	7	US-10-449-902-48020	Sequence 48020, A	354	154.5	4.9	877	7	US-11-389-343-1097	Sequence 1097, Ap
279	163	5.2	753	7	US-11-129-648-13	Sequence 13, Appl	355	154.5	4.9	877	7	US-11-389-343-1100	Sequence 1100, Ap
280	162	5.2	661	7	US-11-371-354-67147	Sequence 67147, A	356	154.5	4.9	877	7	US-11-389-343-1102	Sequence 1102, Ap
281	161	5.1	409	7	US-11-520-715-71047	Sequence 71047, A	357	154.5	4.9	877	7	US-11-389-343-1104	Sequence 1104, Ap
282	160.5	5.1	519	6	US-10-537-102-16	Sequence 16, Appl	358	154.5	4.9	877	7	US-11-389-343-1106	Sequence 1106, Ap
283	160.5	5.1	640	6	US-10-537-102-10	Sequence 10, Appl	359	154.5	4.9	877	7	US-11-389-017-1097	Sequence 1097, Ap
284	160	5.1	470	7	US-11-520-715-64807	Sequence 64807, A	360	154.5	4.9	877	7	US-11-389-017-1100	Sequence 1100, Ap
285	160	5.1	599	7	US-11-056-3558-91592	Sequence 91592, A	361	154.5	4.9	877	7	US-11-389-017-1102	Sequence 1102, Ap
286	160	5.1	599	7	US-11-056-3558-95348	Sequence 95348, A	362	154.5	4.9	877	7	US-11-389-017-1104	Sequence 1104, Ap
287	160	5.1	634	7	US-11-056-3558-91591	Sequence 91591, A	363	154.5	4.9	877	7	US-11-389-017-1106	Sequence 1106, Ap
288	160	5.1	634	7	US-11-056-3558-95347	Sequence 95347, A	364	154.5	4.9	1192	7	US-11-056-3558-46297	Sequence 46297, A
289	160	5.1	744	7	US-11-056-3558-91590	Sequence 91590, A	365	154.5	4.9	2517	7	US-11-283-329-204	Sequence 204, Appl
290	160	5.1	744	7	US-11-056-3558-95346	Sequence 95346, A	366	154.5	4.9	461	6	US-10-953-349-24311	Sequence 24311, A
291	160	5.1	1479	6	US-10-525-573-325	Sequence 325, Appl	367	154	4.9	461	7	US-11-056-3558-55336	Sequence 55336, A
292	159.5	5.1	494	7	US-11-056-3558-97011	Sequence 97011, A	368	154	4.9	492	6	US-10-953-349-24310	Sequence 24310, A
293	159	5.1	396	6	US-10-449-902-43379	Sequence 43379, A	369	154	4.9	492	7	US-11-056-3558-52535	Sequence 52535, A
294	159	5.1	543	6	US-10-449-902-55599	Sequence 55599, A	370	154	4.9	1010	7	US-11-056-3558-78678	Sequence 78678, A
295	159	5.1	985	6	US-10-574-398-277	Sequence 277, Appl	371	154	4.9	1090	7	US-11-056-3558-78677	Sequence 78677, A
296	158.5	5.1	912	7	US-11-056-3558-87717	Sequence 87717, A	372	153.5	4.9	775	7	US-11-056-3558-88930	Sequence 88930, A
297	158.5	5.1	993	7	US-11-056-3558-87716	Sequence 87716, A	373	153.5	4.9	775	7	US-11-056-3558-92686	Sequence 92686, A
298	158.5	5.1	1032	7	US-11-368-333-32	Sequence 32, Appl	374	153.5	4.9	854	7	US-11-389-343-1111	Sequence 1111, Ap
299	158.5	5.1	1032	7	US-11-368-334-31	Sequence 31, Appl	375	153.5	4.9	854	7	US-11-389-343-1113	Sequence 1113, Ap
300	158.5	5.1	1070	7	US-11-056-3558-87715	Sequence 87715, A	376	153.5	4.9	854	7	US-11-389-343-1115	Sequence 1115, Ap
301	158	5.0	363	7	US-11-174-307B-4510	Sequence 4510, Ap	377	153.5	4.9	854	7	US-11-389-017-1111	Sequence 1111, Ap
302	157.5	5.0	1069	7	US-11-375-359-123	Sequence 123, Appl	378	153.5	4.9	854	7	US-11-389-017-1113	Sequence 1113, Ap
303	157.5	5.0	1076	7	US-11-090-997-1018	Sequence 1018, Appl	379	153.5	4.9	854	7	US-11-389-017-1115	Sequence 1115, Ap
304	157.5	5.0	1032	7	US-11-341-319-3	Sequence 3, Appl	380	153.5	4.9	854	7	US-11-056-3558-79969	Sequence 79969, A
305	156.5	5.0	503	7	US-11-520-715-65448	Sequence 65448, A	381	153.5	4.9	877	7	US-11-389-343-1110	Sequence 1110, Ap
306	156.5	5.0	551	6	US-10-449-902-36375	Sequence 36375, A	382	153.5	4.9	877	7	US-11-389-343-1112	Sequence 1112, Ap
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313	156.5	5.0	354	6	US-10-219-051B-9717	Sequence 9717, Ap	389	153.5	4.9	894	7	US-11-371-354-63015	Sequence 63015, A
314	156.5	5.0	354	6	US-10-219-051B-9721	Sequence 9721, Ap	390	153.5	4.9	1032	7	US-11-341-319-1	Sequence 1, Appl
315	156	5.0	354	6	US-10-219-051B-9725	Sequence 9725, Ap	391	153.5	4.9	1032	7	US-11-368-333-34	Sequence 34, Appl
316	156	5.0	354	6	US-10-219-051B-9729	Sequence 9729, Ap	392	153.5	4.9	1032	7	US-11-368-334-7	Sequence 7, Appl
317	156	5.0	354	6	US-10-219-051B-9733	Sequence 9733, Ap	393	153.5	4.9	1032	7	US-11-371-354-62183	Sequence 62183, A
318	156	5.0	354	6	US-10-219-051B-9737	Sequence 9737, Ap	394	153.5	4.9	1041	7	US-11-056-3558-96010	Sequence 96010, A
319	156	5.0	445	7	US-11-520-715-64796	Sequence 64796, A	395	153.5	4.9	1055	7	US-11-368-333-36	Sequence 36, Appl
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323	155.5	5.0	877	7	US-11-389-343-1108	Sequence 1108, Ap	399	153	4.9	699	7	US-11-296-571-1	Sequence 1, Appl
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325	155.5	5.0	411	6	US-10-953-349-33758	Sequence 33758, A	401	152.5	4.9	699	7	US-11-395-249-132	Sequence 132, Appl
326	155	4.9	411	6	US-11-056-3558-7403	Sequence 7403, Ap	402	152.5	4.9	699	7	US-11-520-715-63020	Sequence 63020, A
327	155	4.9	411	6	US-10-953-349-33757	Sequence 33757, A	403	152	4.8	616	7	US-11-520-715-65688	Sequence 65688, A
328	155	4.9	412	6	US-11-056-3558-7402	Sequence 7402, Ap	404	152	4.8	631	7	US-11-520-715-65688	Sequence 65688, A
329	155	4.9	412	6	US-11-056-3558-19208	Sequence 19208, A	405	152	4.8	682	6	US-10-449-902-35729	Sequence 35729, A
330	155	4.9	504	6	US-10-537-102-6	Sequence 6, Appl	406	152	4.8	682	6	US-10-449-902-55720	Sequence 55720, A
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332	155	4.9	1041	7	US-11-368-333-26	Sequence 26, Appl	408	151.5	4.8	629	6	US-10-537-102-12	Sequence 12, Appl
333	155	4.9	1041	7	US-11-368-334-26	Sequence 26, Appl	409	151	4.8	470	6	US-10-449-902-43319	Sequence 43319, A
334	155	4.9	1054	7	US-11-387-182-6	Sequence 6, Appl	410	150.5	4.8	1061	6	US-10-449-902-41173	Sequence 41173, A
335	155	4.9	1059	7	US-11-368-333-30	Sequence 30, Appl	411	150.5	4.8	1109	7	US-11-330-403-3817	Sequence 3817, Ap
336	155	4.9	1059	7	US-11-387-182-8	Sequence 8, Appl	412	150.5	4.8	1109	7	US-11-330-403-9397	Sequence 9397, Ap
337	155	4.9	376	6	US-10-219-051B-13992	Sequence 13992, A	413	150	4.8	259	6	US-10-970-823-71	Sequence 71, Appl
338	154.5	4.9	376	6	US-10-405-027-4069	Sequence 4069, Ap	414	150	4.8	259	6	US-11-371-354-66133	Sequence 66133, A
339	154.5	4.9	376	6	US-11-371-354-65777	Sequence 65777, A	415	150	4.8	367	7	US-11-105-233-62	Sequence 62, Appl
340	154.5	4.9	514	7	US-11-174-307B-4396	Sequence 4396, Ap	416	150	4.8	367	7	US-11-371-354-64927	Sequence 64927, A
341	154.5	4.9	854	7	US-11-389-343-1098	Sequence 1098, Ap	417	150	4.8	1294	6	US-10-612-783-6698	Sequence 6698, Ap
342	154.5	4.9	854	7	US-11-389-343-1101	Sequence 1101, Ap	418	149.5	4.8	1294	6	US-11-520-715-69853	Sequence 69853, A
343	154.5	4.9	854	7	US-11-389-343-1103	Sequence 1103, Ap	419	149.5	4.8	574	7	US-10-449-902-41026	Sequence 41026, A
344	154.5	4.9	854	7	US-11-389-343-1105	Sequence 1105, Ap	420	149.5	4.8	848	6	US-10-449-902-36640	Sequence 36640, A
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422	149	4.8	419	6	US-10-449-902-38614	Sequence 38614, A	497	143.5	4.6	935	6	US-10-449-902-46779	Sequence 46779, A
423	149	4.8	444	7	US-11-056-355B-106189	Sequence 106189, A	498	143.5	4.6	1208	7	US-11-090-997-6	Sequence 6, Appl1
424	149	4.8	444	7	US-11-056-355B-117428	Sequence 117428, A	499	143.5	4.6	1403	7	US-11-520-715-54518	Sequence 54518, A
425	149	4.8	471	7	US-11-056-355B-106188	Sequence 106188, A	500	143.5	4.6	1616	6	US-10-533-519-52	Sequence 52, Appl
426	149	4.8	471	7	US-11-056-355B-117427	Sequence 117427, A	501	143	4.6	1616	6	US-10-533-519-52	Sequence 52, Appl
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428	149	4.8	477	7	US-11-056-355B-117426	Sequence 117426, A	503	142.5	4.5	827	6	US-10-449-902-41294	Sequence 41294, A
429	149	4.8	477	7	US-11-520-715-71314	Sequence 71314, A	504	142	4.5	402	7	US-11-371-354-62467	Sequence 62467, A
430	149	4.8	708	7	US-11-520-715-55435	Sequence 55435, A	505	142	4.5	699	7	US-11-296-571-13	Sequence 13, Appl
431	149	4.8	1504	6	US-10-505-528-662	Sequence 528662, A	506	142	4.5	906	6	US-10-612-783-6193	Sequence 6193, Ap
432	149	4.8	1504	6	US-10-533-519-331	Sequence 331, App	507	141.5	4.5	460	7	US-11-056-355B-46185	Sequence 46185, A
433	149	4.8	1522	6	US-10-570-909-105	Sequence 105, App	508	141.5	4.5	462	7	US-11-056-355B-46184	Sequence 46184, A
434	148.5	4.7	376	6	US-10-219-051B-13990	Sequence 13990, A	509	141.5	4.5	475	7	US-11-056-355B-46183	Sequence 46183, A
435	148.5	4.7	511	6	US-10-449-902-44072	Sequence 44072, A	510	141.5	4.5	575	7	US-11-520-715-47357	Sequence 47357, A
436	148	4.7	699	7	US-11-236-571-11	Sequence 11, Appl	511	141.5	4.5	690	7	US-11-296-571-13	Sequence 13, Appl
437	147.5	4.7	386	7	US-11-056-355B-78532	Sequence 78532, A	512	141.5	4.5	1052	6	US-10-449-902-46489	Sequence 46489, A
438	147.5	4.7	398	7	US-11-056-355B-78531	Sequence 78531, A	513	141.5	4.5	1084	6	US-10-449-902-52915	Sequence 52915, A
439	147.5	4.7	445	7	US-11-056-355B-89859	Sequence 89859, A	514	141	4.5	437	7	US-11-520-715-57154	Sequence 57154, A
440	147.5	4.7	445	7	US-11-056-355B-89859	Sequence 89859, A	515	140.5	4.5	453	6	US-10-953-349-10988	Sequence 10988, A
441	147.5	4.7	452	7	US-11-056-355B-78530	Sequence 78530, A	516	140.5	4.5	533	6	US-10-953-349-10987	Sequence 10987, A
442	147.5	4.7	499	7	US-11-056-355B-89858	Sequence 89858, A	517	140.5	4.5	568	7	US-11-357-421-187	Sequence 187, App
443	147.5	4.7	499	7	US-11-056-355B-93614	Sequence 93614, A	518	140.5	4.5	656	6	US-10-449-902-38110	Sequence 38110, A
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445	147.5	4.7	521	7	US-11-056-355B-93613	Sequence 93613, A	520	140.5	4.5	757	7	US-11-226-554-135	Sequence 135, App
446	147.5	4.7	557	6	US-10-449-902-31160	Sequence 31160, A	521	140.5	4.5	757	7	US-11-248-718-135	Sequence 135, App
447	147.5	4.7	964	6	US-10-449-902-47345	Sequence 47345, A	522	140.5	4.5	757	7	US-11-248-718-135	Sequence 135, App
448	147	4.7	685	7	US-11-520-715-57941	Sequence 57941, A	523	140.5	4.5	757	7	US-11-486-332-12	Sequence 12, Appl
449	147	4.7	2414	7	US-11-283-329-176	Sequence 176, App	524	140.5	4.5	953	7	US-11-056-355B-107904	Sequence 107904, A
450	146.5	4.7	925	7	US-11-056-355B-70331	Sequence 70331, A	525	140.5	4.5	953	7	US-11-056-355B-119143	Sequence 119143, A
451	146	4.7	293	6	US-10-953-349-22365	Sequence 22365, A	526	140.5	4.5	958	7	US-11-056-355B-46620	Sequence 46620, A
452	146	4.7	439	6	US-10-500-477A-15	Sequence 15, Appl	527	140.5	4.5	1009	7	US-11-056-355B-46619	Sequence 46619, A
453	146	4.7	748	6	US-10-953-349-3827	Sequence 3827, Ap	528	140.5	4.5	1016	7	US-11-056-355B-46618	Sequence 46618, A
454	146	4.7	785	6	US-10-953-349-3826	Sequence 3826, Ap	529	140	4.5	277	7	US-11-371-354-69075	Sequence 69075, A
455	146	4.7	885	6	US-10-505-528-432	Sequence 432, App	530	140	4.5	754	7	US-11-056-355B-68915	Sequence 68915, A
456	146	4.7	885	6	US-11-251-465-20	Sequence 20, Appl	531	140	4.5	883	7	US-11-056-355B-81300	Sequence 81300, A
457	146	4.7	978	6	US-10-953-349-9199	Sequence 9199, Ap	532	140	4.5	943	7	US-11-056-355B-81299	Sequence 81299, A
458	146	4.7	1173	6	US-10-953-349-9198	Sequence 9198, Ap	533	140	4.5	999	7	US-11-330-403-17817	Sequence 17817, A
459	146	4.7	1413	6	US-10-612-783-7027	Sequence 7027, Ap	534	140	4.5	1029	7	US-11-056-355B-81298	Sequence 81298, A
460	145.5	4.6	352	6	US-10-449-902-32358	Sequence 32358, A	535	140	4.5	2014	7	US-11-399-791-18	Sequence 18, Appl
461	145.5	4.6	352	6	US-10-449-902-32813	Sequence 32813, A	536	139.5	4.4	439	7	US-11-056-355B-79833	Sequence 79833, A
462	145.5	4.6	352	6	US-10-449-902-44462	Sequence 44462, A	537	139.5	4.4	451	7	US-11-056-355B-79832	Sequence 79832, A
463	145.5	4.6	827	6	US-10-449-902-54991	Sequence 54991, A	538	139.5	4.4	453	6	US-10-953-349-22994	Sequence 22994, A
464	145.5	4.6	1189	6	US-10-540-844-2	Sequence 4, Appl1	539	139.5	4.4	453	7	US-11-056-355B-59558	Sequence 59558, A
465	145.5	4.6	1236	6	US-10-540-844-2	Sequence 2, Appl1	540	139.5	4.4	467	6	US-10-953-349-22993	Sequence 22993, A
466	145	4.6	292	7	US-11-056-355B-15849	Sequence 15849, A	541	139.5	4.4	467	7	US-11-056-355B-59557	Sequence 59557, A
467	145	4.6	338	7	US-11-105-233-144	Sequence 144, App	542	139.5	4.4	470	6	US-10-953-349-22992	Sequence 22992, A
468	145	4.6	338	7	US-11-371-354-74781	Sequence 74781, A	543	139.5	4.4	470	7	US-11-056-355B-59556	Sequence 59556, A
469	145	4.6	338	7	US-11-510-530-119	Sequence 119, App	544	139.5	4.4	506	7	US-11-056-355B-79831	Sequence 79831, A
470	145	4.6	454	7	US-11-056-355B-56389	Sequence 56389, A	545	139.5	4.4	797	6	US-10-540-898-663	Sequence 663, App
471	145	4.6	518	7	US-11-056-355B-56388	Sequence 56388, A	546	139	4.4	449	7	US-11-251-465-68	Sequence 68, Appl
472	145	4.6	540	7	US-11-056-355B-56387	Sequence 56387, A	547	139	4.4	449	6	US-10-700-439-178	Sequence 178, App
473	145	4.6	553	7	US-11-056-355B-15848	Sequence 15848, A	548	139	4.4	5179	6	US-10-541-749-151	Sequence 151, App
474	145	4.6	971	6	US-10-449-902-52625	Sequence 52625, A	549	139	4.4	5179	6	US-10-219-051B-10430	Sequence 10430, A
475	145	4.6	1032	7	US-11-341-319-2	Sequence 2, Appl1	550	139	4.4	5179	6	US-10-219-051B-13789	Sequence 13789, A
476	145	4.6	1032	7	US-11-368-333-38	Sequence 38, Appl	551	139	4.4	5179	7	US-11-105-233-185	Sequence 185, App
477	145	4.6	1032	7	US-11-368-334-9	Sequence 9, Appl1	552	138.5	4.4	660	6	US-10-449-902-36212	Sequence 36212, A
478	144.5	4.6	841	7	US-11-375-359-124	Sequence 124, App	553	138.5	4.4	863	7	US-11-520-715-60549	Sequence 60549, A
479	144.5	4.6	906	6	US-10-511-795-4	Sequence 4, Appl1	554	138.5	4.4	1005	7	US-11-520-715-60549	Sequence 60549, A
480	144.5	4.6	1356	6	US-11-214-063A-1338	Sequence 1338, Ap	555	138	4.4	1005	7	US-11-486-321-109	Sequence 63864, A
481	144.5	4.6	661	7	US-11-486-321-10	Sequence 10, Appl	556	138	4.4	322	7	US-11-371-354-63773	Sequence 109, App
482	144	4.6	661	7	US-10-449-902-53937	Sequence 53937, A	557	138	4.4	322	7	US-10-449-902-48447	Sequence 48447, A
483	144	4.6	1072	6	US-11-056-355B-106706	Sequence 106706, A	558	138	4.4	675	6	US-10-449-902-50618	Sequence 50618, A
484	144	4.6	431	7	US-11-056-355B-106705	Sequence 106705, A	559	138	4.4	675	6	US-10-528-2608-217	Sequence 217, App
485	143.5	4.6	431	7	US-11-056-355B-106706	Sequence 106706, A	560	138	4.4	858	6	US-11-466-372-2528	Sequence 2528, Ap
486	143.5	4.6	431	7	US-11-056-355B-117945	Sequence 117945, A	561	138	4.4	1003	7	US-11-166-372-2528	Sequence 2528, Ap
487	143.5	4.6	450	7	US-11-056-355B-106705	Sequence 106705, A	562	138	4.4	1003	7	US-11-537-102-33	Sequence 33, Appl
488	143.5	4.6	450	7	US-11-056-355B-106705	Sequence 106705, A	563	137.5	4.4	207	7	US-11-174-307B-5004	Sequence 5004, Ap
489	143.5	4.6	496	7	US-11-056-355B-106704	Sequence 106704, A	564	137	4.4	412	7	US-11-056-355B-15925	Sequence 15925, A
490	143.5	4.6	496	7	US-11-056-355B-117943	Sequence 117943, A	565	137	4.4	412	7	US-11-265-762-116	Sequence 116, App
491	143.5	4.6	603	7	US-11-056-355B-88145	Sequence 88145, A	566	137	4.4	497	7	US-10-449-902-45586	Sequence 45586, A
492	143.5	4.6	603	7	US-11-056-355B-79474	Sequence 79474, A	567	137	4.4	973	6	US-10-449-902-56147	Sequence 56147, A
493	143.5	4.6	605	7	US-11-056-355B-88144	Sequence 88144, A	568	137	4.4	1059	6	US-10-530-393-5	Sequence 5, Appl1
494	143.5	4.6	611	7	US-11-056-355B-79473	Sequence 79473, A	569	137	4.4	4544	6	US-10-449-902-54204	Sequence 54204, A
495	143.5	4.6	613	6	US-10-521-518-51	Sequence 51, Appl	570	136.5	4.4	161	6	US-10-449-902-41243	Sequence 41243, A
496	143.5	4.6	613	7	US-11-056-355B-79472	Sequence 79472, A	571	136.5	4.4	535	6	US-10-449-902-41243	Sequence 41243, A

572	136.5	4.4	688	7	US-11-296-571-12	Sequence 13, Appl	645	131	4.2	493	7	US-11-520-715-64117	Sequence 64117, A
573	136.5	4.4	775	7	US-11-520-715-56330	Sequence 56330, A	646	131	4.2	766	6	US-10-449-902-36778	Sequence 36778, A
574	136	4.3	322	7	US-11-246-999-79	Sequence 79, Appl	647	131	4.2	938	7	US-11-330-403-10157	Sequence 10157, A
575	136	4.3	586	6	US-10-449-902-51689	Sequence 51689, A	648	131	4.2	1024	7	US-11-317-789A-403	Sequence 403, App
576	136	4.3	737	7	US-11-486-332-14	Sequence 14, Appl	649	131	4.2	1074	6	US-10-449-902-52953	Sequence 52953, A
577	136	4.3	4465	6	US-10-669-920-477	Sequence 477, App	650	130.5	4.2	1177	7	US-11-056-355B-9410	Sequence 9410, Ap
578	136	4.3	4523	6	US-10-669-920-472	Sequence 472, App	651	130.5	4.2	450	6	US-10-449-902-43069	Sequence 43069, A
579	135.5	4.3	406	6	US-10-953-349-31643	Sequence 31643, A	652	130.5	4.2	2003	7	US-11-364-243-8	Sequence 8, Appl
580	135.5	4.3	406	6	US-10-953-349-31643	Sequence 31643, A	653	130	4.1	286	7	US-11-056-355B-95411	Sequence 95411, A
581	135.5	4.3	427	6	US-10-219-051B-6490	Sequence 6490, Ap	654	130	4.1	296	7	US-11-056-355B-95411	Sequence 95411, A
582	135.5	4.3	440	7	US-11-251-465-65	Sequence 65, Appl	655	130	4.1	389	7	US-11-056-355B-91654	Sequence 91654, A
583	135.5	4.3	464	7	US-11-056-355B-91633	Sequence 91633, A	656	130	4.1	399	7	US-11-056-355B-95410	Sequence 95410, A
584	135.5	4.3	464	7	US-11-056-355B-95389	Sequence 95389, A	657	130	4.1	488	6	US-10-574-398-372	Sequence 372, App
585	135.5	4.3	493	7	US-11-056-355B-91632	Sequence 91632, A	658	130	4.1	639	7	US-11-090-997-1778	Sequence 1778, Ap
586	135.5	4.3	493	7	US-11-056-355B-95388	Sequence 95388, A	659	130	4.1	639	7	US-11-293-697-3849	Sequence 3849, Ap
587	135.5	4.3	743	7	US-11-121-133-164	Sequence 164, App	660	130	4.1	758	7	US-11-520-715-72684	Sequence 72684, A
588	135.5	4.3	743	7	US-11-121-133-254	Sequence 254, App	661	130	4.1	915	6	US-10-523-014-4	Sequence 4, Appl
589	135.5	4.3	998	7	US-11-330-403-13357	Sequence 13357, A	662	129.5	4.1	395	7	US-11-520-715-55129	Sequence 55129, A
590	135.5	4.3	1012	6	US-10-953-349-13624	Sequence 13624, A	663	129.5	4.1	637	7	US-11-520-715-44109	Sequence 44109, A
591	135.5	4.3	1025	6	US-10-953-349-13623	Sequence 13623, A	664	129.5	4.1	806	7	US-11-056-355B-78679	Sequence 78679, A
592	135	4.3	696	7	US-11-166-372-2425	Sequence 2425, Ap	665	129.5	4.1	1240	7	US-11-434-137-8228	Sequence 8228, Ap
593	134.5	4.3	519	7	US-11-520-715-52816	Sequence 52816, A	666	129.5	4.1	1240	7	US-11-434-184-8228	Sequence 8228, Ap
594	134.5	4.3	638	6	US-10-612-783-3978	Sequence 3978, Ap	667	129.5	4.1	1240	7	US-11-434-199-8228	Sequence 8228, Ap
595	134.5	4.3	812	7	US-11-056-355B-96011	Sequence 96011, A	668	129.5	4.1	1240	7	US-11-434-203-8228	Sequence 8228, Ap
596	134.5	4.3	847	7	US-11-056-355B-79588	Sequence 79588, A	669	129.5	4.1	1240	7	US-11-434-127-8228	Sequence 8228, Ap
597	134.5	4.3	1009	6	US-10-538-002-135	Sequence 135, App	670	129.5	4.1	1275	6	US-10-548-463-223	Sequence 223, App
598	134.5	4.3	2240	6	US-10-544-731-4	Sequence 4, Appl	671	129.5	4.1	1275	6	US-10-513-024-1232	Sequence 1232, Ap
599	134.5	4.3	2258	6	US-10-544-731-3	Sequence 3, Appl	672	129	4.1	226	7	US-11-520-715-56586	Sequence 56586, A
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601	134	4.3	476	7	US-11-056-355B-16525	Sequence 16525, A	674	129	4.1	291	7	US-11-520-715-47180	Sequence 47180, A
602	134	4.3	502	7	US-11-174-307B-5262	Sequence 5262, Ap	676	129	4.1	647	7	US-11-520-715-55118	Sequence 55118, A
603	134	4.3	697	6	US-10-449-902-50662	Sequence 50662, A	677	129	4.1	652	6	US-10-953-349-5551	Sequence 5551, Ap
604	134	4.3	921	6	US-10-519-135-6	Sequence 6, Appl	678	129	4.1	652	7	US-11-056-355B-30482	Sequence 30482, A
605	133.5	4.3	239	7	US-11-293-697-2474	Sequence 2474, Ap	679	129	4.1	652	7	US-11-056-355B-97017	Sequence 97017, A
606	133.5	4.3	239	7	US-11-293-697-2850	Sequence 2850, Ap	680	129	4.1	651	7	US-11-056-355B-97017	Sequence 97017, A
607	133.5	4.3	239	7	US-11-371-354-67705	Sequence 67705, A	681	129	4.1	752	7	US-11-520-715-49546	Sequence 49546, A
608	133.5	4.3	239	7	US-11-371-354-77116	Sequence 77116, A	682	129	4.1	818	7	US-11-415-063-10	Sequence 10, Appl
609	133.5	4.3	288	6	US-10-449-902-40102	Sequence 40102, A	683	129	4.1	1040	7	US-11-056-355B-88229	Sequence 88229, A
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611	133.5	4.3	4464	6	US-10-530-393-8	Sequence 8, Appl	685	129	4.1	1126	7	US-11-293-697-3665	Sequence 3665, Ap
612	133.5	4.3	4464	6	US-10-530-393-10	Sequence 10, Appl	686	129	4.1	1210	7	US-11-056-355B-88228	Sequence 88228, A
613	133	4.2	694	7	US-11-056-355B-72373	Sequence 72373, A	687	129	4.1	1210	7	US-11-056-355B-91984	Sequence 91984, A
614	133	4.2	932	6	US-10-519-135-8	Sequence 8, Appl	688	129	4.1	2000	6	US-10-533-519-674	Sequence 674, App
615	133	4.2	1564	7	US-11-214-063A-1254	Sequence 1254, Ap	689	129	4.1	2074	7	US-11-165-586-21	Sequence 21, Appl
616	133	4.2	4391	7	US-11-183-325-56	Sequence 56, Appl	690	129	4.1	2321	6	US-10-518-751-8	Sequence 8, Appl
617	132.5	4.2	332	7	US-11-246-999-32	Sequence 32, Appl	691	128.5	4.1	291	7	US-11-520-715-64637	Sequence 64637, A
618	132.5	4.2	426	7	US-11-090-997-286	Sequence 286, App	692	128.5	4.1	348	6	US-10-540-808-5	Sequence 5, Appl
619	132.5	4.2	434	6	US-10-545-557-1	Sequence 1, Appl	693	128.5	4.1	348	6	US-10-540-808-6	Sequence 6, Appl
620	132.5	4.2	463	6	US-10-496-087A-1	Sequence 1, Appl	694	128.5	4.1	429	7	US-11-520-715-42749	Sequence 42749, A
621	132.5	4.2	463	7	US-11-090-997-284	Sequence 284, App	695	128.5	4.1	671	6	US-10-449-902-52071	Sequence 52071, A
622	132.5	4.2	587	7	US-11-030-653-32	Sequence 32, Appl	696	128.5	4.1	697	6	US-10-953-349-3828	Sequence 3828, Ap
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624	132.5	4.2	718	7	US-11-056-355B-79589	Sequence 79589, A	698	128.5	4.1	803	7	US-11-056-355B-95191	Sequence 95191, A
625	132.5	4.2	838	7	US-11-520-715-58433	Sequence 58433, A	699	128.5	4.1	821	7	US-11-343-271-48	Sequence 48, Appl
626	132.5	4.2	1498	7	US-11-214-063A-1322	Sequence 1322, Ap	700	128.5	4.1	925	7	US-11-293-697-3889	Sequence 3889, Ap
627	132	4.2	717	7	US-11-056-355B-71164	Sequence 71164, A	701	128.5	4.1	962	6	US-10-449-902-52324	Sequence 52324, A
628	132	4.2	891	6	US-10-449-902-53978	Sequence 53978, A	702	128.5	4.1	985	7	US-11-056-355B-88230	Sequence 88230, A
629	132	4.2	891	6	US-10-449-902-56281	Sequence 56281, A	703	128.5	4.1	985	7	US-11-056-355B-91986	Sequence 91986, A
630	132	4.2	979	6	US-10-219-051B-2016	Sequence 2016, Ap	704	128.5	4.1	1133	6	US-10-533-519-1705	Sequence 1705, Ap
631	132	4.2	979	6	US-10-219-051B-3079	Sequence 3079, Ap	705	128.5	4.1	1460	7	US-11-247-437-14	Sequence 14, Appl
632	132	4.2	979	6	US-10-219-051B-3083	Sequence 3083, Ap	706	128	4.1	213	7	US-11-056-355B-1607	Sequence 1607, Ap
633	132	4.2	979	6	US-10-219-051B-3087	Sequence 3087, Ap	707	128	4.1	213	7	US-11-056-355B-8787	Sequence 8787, Ap
634	132	4.2	979	6	US-10-219-051B-3091	Sequence 3091, Ap	708	128	4.1	280	7	US-11-056-355B-1606	Sequence 1606, Ap
635	132	4.2	979	6	US-10-219-051B-10711	Sequence 10711, A	709	128	4.1	367	7	US-11-056-355B-8785	Sequence 8785, Ap
636	132	4.2	979	7	US-11-232-404-43	Sequence 43, Appl	710	128	4.1	707	7	US-11-520-715-55449	Sequence 55449, A
637	132	4.2	979	7	US-11-403-580-3	Sequence 3, Appl	711	128	4.1	998	7	US-11-330-403-13360	Sequence 13360, A
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639	132	4.2	987	7	US-11-330-403-13361	Sequence 13361, A	713	128	4.1	1145	7	US-11-330-403-7343	Sequence 7343, Ap
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641	131.5	4.2	636	7	US-11-520-715-45755	Sequence 45755, A	715	127.5	4.1	544	7	US-11-056-355B-2962	Sequence 2962, Ap
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643	131	4.2	213	6	US-10-449-902-51210	Sequence 51210, A	717	127.5	4.1	749	7	US-11-293-697-4038	Sequence 4038, Ap
644	131	4.2	492	7	US-11-520-715-72327	Sequence 72327, A	718	127.5	4.1	750	7	US-11-056-355B-46834	Sequence 46834, A

719	127.5	4.1	750	7	US-11-056-355B-91032	Sequence 91032, A	797	125	4.0	293	6	US-10-953-349-31470	Sequence 31470, A
720	127.5	4.1	750	7	US-11-056-355B-94788	Sequence 94788, A	798	125	4.0	678	6	US-10-219-051B-2092	Sequence 2092, Ap
721	127.5	4.1	768	7	US-11-056-355B-46833	Sequence 46833, A	799	125	4.0	690	7	US-11-330-403-4347	Sequence 4347, Ap
722	127.5	4.1	768	7	US-11-056-355B-91031	Sequence 91031, A	800	125	4.0	706	6	US-10-449-902-44028	Sequence 44028, A
723	127.5	4.1	768	7	US-11-056-355B-94787	Sequence 94787, A	801	125	4.0	763	7	US-11-056-355B-107905	Sequence 107905,
724	127.5	4.1	860	7	US-11-056-355B-46832	Sequence 46832, A	802	125	4.0	763	7	US-11-056-355B-119144	Sequence 119144,
725	127.5	4.1	860	7	US-11-056-355B-91030	Sequence 91030, A	803	125	4.0	775	6	US-10-805-394-3773	Sequence 3773, Ap
726	127.5	4.1	860	7	US-11-056-355B-94786	Sequence 94786, A	804	125	4.0	917	6	US-10-504-973-26	Sequence 26, Appl
727	127.5	4.1	905	7	US-11-056-355B-46299	Sequence 46299, A	805	125	4.0	2026	6	US-10-309-407-86	Sequence 86, Appl
728	127.5	4.1	948	7	US-11-056-355B-83031	Sequence 83031, A	806	125	4.0	2144	7	US-11-283-329-160	Sequence 160, App
729	127.5	4.1	1000	7	US-11-056-355B-46298	Sequence 46298, A	807	124.5	4.0	298	6	US-10-154-678-22	Sequence 22, Appl
730	127.5	4.1	1010	7	US-11-056-355B-83030	Sequence 83030, A	808	124.5	4.0	298	6	US-10-405-027-4001	Sequence 4001, Ap
731	127.5	4.1	1120	7	US-11-056-355B-83029	Sequence 83029, A	809	124.5	4.0	298	6	US-10-405-027-5409	Sequence 5409, Ap
732	127.5	4.1	1522	6	US-10-502-394-31	Sequence 31, Appl	810	124.5	4.0	298	6	US-10-405-027-5410	Sequence 5410, Ap
733	127	4.1	223	7	US-11-520-715-41681	Sequence 41681, A	811	124.5	4.0	298	6	US-10-405-027-5411	Sequence 5411, Ap
734	127	4.1	224	7	US-11-520-715-64197	Sequence 64197, A	812	124.5	4.0	298	6	US-10-405-027-5412	Sequence 5412, Ap
735	127	4.1	238	7	US-11-286-056-4	Sequence 4, Appl	813	124.5	4.0	298	6	US-10-405-027-5680	Sequence 5680, Ap
736	127	4.1	276	7	US-11-520-715-63885	Sequence 63885, A	814	124.5	4.0	298	6	US-10-405-027-5682	Sequence 5682, Ap
737	127	4.1	324	6	US-10-533-519-2267	Sequence 2267, Ap	815	124.5	4.0	298	7	US-11-297-134-25	Sequence 25, Appl
738	127	4.1	370	7	US-11-520-715-51446	Sequence 51446, A	816	124.5	4.0	298	7	US-11-412-325-22	Sequence 22, Appl
739	127	4.1	773	1	US-09-887-272A-1971	Sequence 1971, Ap	817	124.5	4.0	298	6	US-11-371-354-65571	Sequence 65571, A
740	127	4.1	773	7	US-11-056-355B-97107	Sequence 97107, A	818	124.5	4.0	395	6	US-10-540-898-661	Sequence 661, App
741	127	4.1	986	7	US-11-520-715-43024	Sequence 43024, A	819	124.5	4.0	408	7	US-11-371-354-12765	Sequence 12765, A
742	127	4.1	1073	6	US-10-713-648A-54	Sequence 54, Appl	820	124.5	4.0	408	7	US-11-371-354-65161	Sequence 65161, A
743	127	4.1	1595	6	US-10-486-020-18	Sequence 18, Appl	821	124.5	4.0	428	7	US-11-520-715-45741	Sequence 45741, A
744	127	4.1	1614	7	US-11-056-355B-88827	Sequence 88827, A	824	124.5	4.0	546	6	US-10-970-823-250	Sequence 250, App
745	127	4.1	1614	7	US-11-056-355B-92583	Sequence 92583, A	825	124.5	4.0	685	7	US-11-090-997-1988	Sequence 1988, Ap
746	127	4.1	1660	7	US-11-056-355B-88826	Sequence 88826, A	826	124.5	4.0	884	6	US-10-449-902-53270	Sequence 53270, A
747	127	4.1	1660	7	US-11-056-355B-92582	Sequence 92582, A	827	124.5	4.0	903	7	US-11-090-997-1990	Sequence 1990, Ap
748	127	4.1	1828	7	US-11-056-355B-88825	Sequence 88825, A	828	124.5	4.0	929	7	US-11-090-997-1986	Sequence 1986, Ap
749	127	4.1	1828	7	US-11-056-355B-92581	Sequence 92581, A	829	124.5	4.0	999	6	US-10-519-135-4	Sequence 4, Appl
750	127	4.1	1842	7	US-11-056-355B-82005	Sequence 82005, A	830	124.5	4.0	1252	7	US-11-056-355B-44895	Sequence 44895, A
751	127	4.1	1850	7	US-11-056-355B-82004	Sequence 82004, A	831	124.5	4.0	2556	7	US-11-264-243-6	Sequence 6, Appl
752	127	4.1	1895	7	US-11-056-355B-82003	Sequence 82003, A	832	124	4.0	145	6	US-10-537-102-37	Sequence 37, Appl
753	127	4.1	2494	6	US-10-669-920-22	Sequence 22, Appl	833	124	4.0	351	7	US-11-056-355B-65587	Sequence 65587, A
754	126.5	4.0	262	7	US-11-056-355B-50250	Sequence 50250, A	834	124	4.0	445	7	US-11-371-354-12335	Sequence 12335, A
757	126.5	4.0	610	7	US-11-090-997-428	Sequence 428, App	835	124	4.0	445	7	US-11-371-354-76145	Sequence 76145, A
758	126.5	4.0	638	6	US-10-449-902-56142	Sequence 56142, A	836	124	4.0	739	7	US-11-056-355B-79347	Sequence 79347, A
760	126.5	4.0	685	7	US-11-175-714-2	Sequence 2, Appl	837	124	4.0	739	7	US-11-056-355B-84020	Sequence 84020, A
761	126.5	4.0	685	7	US-11-175-714-28	Sequence 28, Appl	838	124	4.0	766	7	US-11-056-355B-79346	Sequence 79346, A
762	126.5	4.0	685	7	US-11-175-714-32	Sequence 32, Appl	839	124	4.0	766	7	US-11-056-355B-84019	Sequence 84019, A
763	126.5	4.0	685	7	US-11-175-714-34	Sequence 34, Appl	840	124	4.0	768	7	US-11-056-355B-84018	Sequence 84018, A
764	126.5	4.0	685	7	US-11-175-714-36	Sequence 36, Appl	841	124	4.0	800	7	US-11-056-355B-91076	Sequence 91076, A
765	126.5	4.0	685	7	US-11-175-714-38	Sequence 38, Appl	842	124	4.0	800	7	US-11-056-355B-94832	Sequence 94832, A
766	126.5	4.0	685	7	US-11-178-724-20	Sequence 20, Appl	843	124	4.0	839	6	US-10-449-902-49998	Sequence 49998, A
767	126.5	4.0	685	7	US-11-264-243-2	Sequence 2, Appl	844	124	4.0	839	6	US-10-449-902-53600	Sequence 53600, A
768	126.5	4.0	685	7	US-11-071-796A-19	Sequence 19, Appl	845	124	4.0	891	7	US-11-056-355B-91075	Sequence 91075, A
769	126.5	4.0	685	7	US-11-188-417A-20	Sequence 20, Appl	846	124	4.0	891	7	US-11-056-355B-94831	Sequence 94831, A
770	126.5	4.0	685	7	US-11-231-494-20	Sequence 20, Appl	847	124	4.0	1011	7	US-11-056-355B-91074	Sequence 91074, A
771	126.5	4.0	718	6	US-10-449-902-53348	Sequence 53348, A	848	124	4.0	1011	7	US-11-056-355B-94830	Sequence 94830, A
772	126.5	4.0	970	6	US-10-538-002-131	Sequence 131, App	849	124	4.0	1035	6	US-10-449-902-55142	Sequence 55142, A
773	126.5	4.0	977	6	US-10-449-902-50081	Sequence 50081, A	850	124	4.0	2617	7	US-11-051-725-14	Sequence 14, Appl
774	126	4.0	670	7	US-11-056-355B-95856	Sequence 95856, A	851	123.5	3.9	324	6	US-10-449-902-34182	Sequence 34182, A
775	126	4.0	720	7	US-11-371-354-60007	Sequence 60007, A	852	123.5	3.9	713	7	US-11-486-332-16	Sequence 16, Appl
776	126	4.0	739	6	US-10-539-328-425	Sequence 425, App	853	123.5	3.9	718	6	US-10-449-902-53522	Sequence 53522, A
777	126	4.0	854	7	US-11-090-997-518	Sequence 518, App	854	123.5	3.9	724	7	US-11-486-332-82	Sequence 82, Appl
778	126	4.0	957	7	US-11-371-354-65363	Sequence 65363, A	855	123.5	3.9	735	7	US-11-486-332-15	Sequence 15, Appl
779	126	4.0	996	7	US-11-293-716-60	Sequence 60, Appl	856	123.5	3.9	737	7	US-11-486-332-13	Sequence 13, Appl
780	126	4.0	1006	6	US-10-449-902-43074	Sequence 43074, A	857	123.5	3.9	748	7	US-11-486-332-13	Sequence 13, Appl
781	126	4.0	1786	6	US-10-519-328-2	Sequence 2, Appl	858	123.5	3.9	754	7	US-11-486-332-13	Sequence 13, Appl
782	126	4.0	1821	6	US-10-505-928-451	Sequence 451, App	859	123.5	3.9	862	7	US-11-520-715-69546	Sequence 69546, A
783	126	4.0	1821	6	US-10-519-328-1	Sequence 1, Appl	860	123.5	3.9	898	7	US-11-056-355B-79052	Sequence 79052, A
784	125.5	4.0	220	6	US-11-056-355B-50251	Sequence 50251, A	861	123.5	3.9	938	6	US-10-533-322A-138	Sequence 138, App
785	125.5	4.0	249	6	US-10-510-953-59	Sequence 59, Appl	862	123.5	3.9	938	6	US-10-449-902-45681	Sequence 45681, A
788	125.5	4.0	324	7	US-11-520-715-58160	Sequence 58160, A	863	123.5	3.9	1002	6	US-10-449-902-41227	Sequence 41227, A
789	125.5	4.0	501	7	US-11-520-715-38856	Sequence 38856, A	864	123.5	3.9	1140	6	US-10-449-902-41227	Sequence 14, Appl
790	125.5	4.0	508	6	US-10-449-902-30106	Sequence 30106, A	865	123.5	3.9	1198	7	US-11-217-997-14	Sequence 9, Appl
791	125.5	4.0	564	7	US-11-056-355B-38683	Sequence 38683, A	866	123.5	3.9	4419	6	US-10-530-393-9	Sequence 11, Appl
792	125.5	4.0	577	7	US-11-056-355B-38682	Sequence 38682, A	867	123.5	3.9	4419	6	US-10-612-783-4717	Sequence 4717, Ap
793	125.5	4.0	686	7	US-11-264-243-4	Sequence 4, Appl	868	123	3.9	220	6	US-10-953-349-16133	Sequence 16133, A
794	125.5	4.0	944	7	US-11-056-355B-96336	Sequence 96336, A	869	123	3.9	441	6	US-11-174-307B-5246	Sequence 5246, Ap
795	125.5	4.0	946	7	US-11-056-355B-96335	Sequence 96335, A	870	123	3.9	441	6	US-10-953-349-16132	Sequence 16132, A
796	125.5	4.0	1003	7	US-11-056-355B-50497	Sequence 50497, A	871	123	3.9	458	6		

872	123	3.9	477	6	US-10-953-349-16131	Sequence 16131, A	945	121.5	3.9	284	7	US-11-056-355B-98134	Sequence 98134, A
873	123	3.9	618	7	US-11-178-724-19	Sequence 19, Appl	946	121.5	3.9	284	7	US-11-056-355B-109373	Sequence 109373, A
874	123	3.9	618	7	US-11-071-796A-18	Sequence 18, Appl	947	121.5	3.9	286	7	US-11-056-355B-98133	Sequence 98133, A
875	123	3.9	618	7	US-11-188-417A-19	Sequence 19, Appl	948	121.5	3.9	286	7	US-11-056-355B-109372	Sequence 109372, A
876	123	3.9	618	7	US-11-231-494-19	Sequence 19, Appl	949	121.5	3.9	306	7	US-11-056-355B-84354	Sequence 84354, A
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878	123	3.9	951	7	US-11-371-354-71389	Sequence 71389, A	951	121.5	3.9	325	7	US-11-056-355B-40921	Sequence 40921, A
879	123	3.9	951	7	US-11-484-719-4	Sequence 4, Appl	952	121.5	3.9	334	7	US-11-056-355B-91924	Sequence 91924, A
880	123	3.9	1396	6	US-10-090-997-1416	Sequence 1416, App	953	121.5	3.9	334	7	US-11-056-355B-95680	Sequence 95680, A
881	123	3.9	1794	6	US-10-475-117-299	Sequence 299, App	954	121.5	3.9	338	7	US-11-056-355B-88896	Sequence 88896, A
882	123	3.9	1799	6	US-10-475-117-149	Sequence 149, App	955	121.5	3.9	338	7	US-11-056-355B-92652	Sequence 92652, A
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885	123	3.9	22152	6	US-10-475-117-315	Sequence 315, App	958	121.5	3.9	351	7	US-11-056-355B-91923	Sequence 91923, A
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890	122.5	3.9	335	7	US-11-293-697-4002	Sequence 4002, App	963	121.5	3.9	367	7	US-11-056-355B-98132	Sequence 98132, A
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893	122.5	3.9	335	7	US-11-371-354-78632	Sequence 78632, A	966	121.5	3.9	395	7	US-11-056-355B-88895	Sequence 88895, A
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896	122.5	3.9	415	7	US-11-056-355B-106168	Sequence 106168, A	969	121.5	3.9	430	7	US-11-056-355B-27332	Sequence 27332, App
897	122.5	3.9	415	7	US-11-056-355B-117407	Sequence 117407, A	970	121.5	3.9	430	7	US-11-056-355B-47881	Sequence 47881, A
898	122.5	3.9	438	7	US-11-371-354-65761	Sequence 65761, A	971	121.5	3.9	430	7	US-11-056-355B-88894	Sequence 88894, A
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900	122.5	3.9	541	6	US-10-449-902-38744	Sequence 38744, A	973	121.5	3.9	432	6	US-10-953-349-5788	Sequence 5788, App
901	122.5	3.9	702	7	US-11-056-355B-85266	Sequence 85266, A	974	121.5	3.9	432	7	US-11-056-355B-27331	Sequence 27331, A
902	122.5	3.9	716	7	US-11-371-354-64669	Sequence 64669, A	975	121.5	3.9	436	7	US-11-056-355B-47880	Sequence 47880, A
903	122.5	3.9	845	7	US-11-520-715-56930	Sequence 56930, A	976	121.5	3.9	436	6	US-10-953-349-5787	Sequence 5787, App
904	122.5	3.9	848	6	US-10-539-228-371	Sequence 371, App	977	121.5	3.9	436	7	US-11-056-355B-27330	Sequence 27330, A
905	122.5	3.9	884	6	US-10-449-902-56049	Sequence 56049, A	978	121.5	3.9	686	7	US-11-175-714-25	Sequence 25, Appl
906	122.5	3.9	1036	6	US-10-533-519-790	Sequence 790, App	979	121.5	3.9	686	7	US-11-175-714-40	Sequence 40, Appl
907	122.5	3.9	1036	7	US-11-248-956-2	Sequence 2, Appl	980	121.5	3.9	686	7	US-11-175-714-42	Sequence 42, Appl
908	122.5	3.9	1036	7	US-11-121-133-255	Sequence 255, App	981	121.5	3.9	686	7	US-11-175-714-44	Sequence 44, Appl
909	122.5	3.9	1036	7	US-11-121-133-256	Sequence 256, App	982	121.5	3.9	686	7	US-11-175-714-46	Sequence 46, Appl
910	122.5	3.9	1154	7	US-11-301-457-23	Sequence 23, Appl	983	121.5	3.9	697	7	US-11-520-715-41545	Sequence 41545, A
911	122.5	3.9	4393	6	US-10-525-573-366	Sequence 366, App	984	121.5	3.9	760	7	US-11-056-355B-47907	Sequence 47907, A
912	122.5	3.9	4393	7	US-11-450-360-1	Sequence 1, Appl	985	121.5	3.9	791	6	US-10-533-519-66	Sequence 66, Appl
913	122.5	3.9	10431	6	US-10-475-117-310	Sequence 310, App	986	121.5	3.9	813	7	US-11-056-355B-37149	Sequence 37149, A
914	122.5	3.9	22152	6	US-10-544-944-1	Sequence 1, Appl	987	121.5	3.9	813	7	US-11-056-355B-37204	Sequence 37204, A
915	122	3.9	269	7	US-11-371-354-67313	Sequence 67313, A	988	121.5	3.9	851	7	US-11-056-355B-37148	Sequence 37148, A
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917	122	3.9	328	7	US-11-293-112-9	Sequence 9, Appl	990	121.5	3.9	863	7	US-11-289-102-215	Sequence 215, App
918	122	3.9	434	6	US-10-449-902-35415	Sequence 35415, A	991	121.5	3.9	863	7	US-11-289-102-264	Sequence 264, App
919	122	3.9	434	6	US-10-449-902-36128	Sequence 36128, A	992	121.5	3.9	902	7	US-11-056-355B-37147	Sequence 37147, A
920	122	3.9	441	7	US-11-371-354-57405	Sequence 57405, A	993	121.5	3.9	902	7	US-11-056-355B-37202	Sequence 37202, A
921	122	3.9	451	6	US-10-219-051B-8271	Sequence 8271, App	994	121.5	3.9	928	7	US-11-520-715-57791	Sequence 57791, A
922	122	3.9	495	7	US-11-174-307B-3112	Sequence 3112, App	995	121.5	3.9	1285	7	US-11-090-997-938	Sequence 938, App
923	122	3.9	575	7	US-11-217-997-32	Sequence 32, Appl	996	121.5	3.9	1332	6	US-10-449-902-41138	Sequence 41138, A
924	122	3.9	633	7	US-11-500-008-5	Sequence 5, Appl	997	121.5	3.9	1408	7	US-11-090-997-942	Sequence 942, App
925	122	3.9	713	6	US-10-540-898-668	Sequence 668, App	998	121.5	3.9	1419	7	US-11-365-989-52	Sequence 52, Appl
926	122	3.9	715	7	US-11-056-355B-85259	Sequence 85259, A	999	121.5	3.9	1419	7	US-11-090-997-940	Sequence 940, App
927	122	3.9	718	7	US-11-056-355B-81584	Sequence 81584, A	1000	121.5	3.9	2265	6	US-10-562-469-11	Sequence 11, Appl
928	122	3.9	733	7	US-11-090-997-332	Sequence 332, App	1001	121	3.9	264	7	US-11-520-715-43726	Sequence 43726, A
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930	122	3.9	1398	7	US-11-217-997-4	Sequence 4, Appl	1003	121	3.9	284	7	US-11-051-725-72	Sequence 72, Appl
931	122	3.9	1403	7	US-11-217-997-12	Sequence 12, Appl	1004	121	3.9	299	6	US-10-953-349-39478	Sequence 39478, A
932	122	3.9	1404	7	US-11-217-997-2	Sequence 2, Appl	1005	121	3.9	239	7	US-11-056-355B-1269	Sequence 1269, App
933	122	3.9	1547	7	US-11-217-997-16	Sequence 16, Appl	1006	121	3.9	522	6	US-10-449-902-44062	Sequence 44062, A
934	122	3.9	1577	7	US-11-217-997-22	Sequence 22, Appl	1007	121	3.9	559	7	US-11-357-421-198	Sequence 198, App
935	122	3.9	1577	7	US-11-217-997-20	Sequence 20, Appl	1008	121	3.9	788	6	US-10-449-902-41167	Sequence 41167, A
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937	122	3.9	1620	7	US-11-217-997-42	Sequence 42, Appl	1010	121	3.9	955	7	US-11-166-372-2652	Sequence 2652, App
938	122	3.9	1653	7	US-11-217-997-40	Sequence 40, Appl	1011	121	3.9	2117	7	US-11-330-403-15081	Sequence 15081, A
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940	122	3.9	2087	6	US-10-669-920-913	Sequence 913, App	1013	121	3.9	2531	6	US-10-219-051B-9649	Sequence 9649, App
941	122	3.9	2203	6	US-10-539-228-726	Sequence 726, App	1014	121	3.9	2531	6	US-10-219-051B-9653	Sequence 9653, App
942	122	3.9	2511	7	US-11-051-725-12	Sequence 12, Appl	1015	121	3.9	2531	6	US-10-219-051B-9657	Sequence 9657, App
943	122	3.9	2511	7	US-11-051-725-13	Sequence 13, Appl	1016	120.5	3.8	256	7	US-11-520-715-50932	Sequence 50932, A
944	122	3.9	2523	7	US-11-051-725-11	Sequence 11, Appl	1017	120.5	3.8	371	7	US-11-371-354-63091	Sequence 63091, A

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1029	120.5	3.8	976	6	US-10-519-135-2	Sequence 2, Appl	1102	119	3.8	784	7	US-11-371-354-62111	Sequence 62111, A
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1032	120.5	3.8	987	6	US-10-953-349-12072	Sequence 12072, A	1105	119	3.8	809	7	US-11-371-354-73463	Sequence 73463, A
1033	120.5	3.8	1003	6	US-11-056-355B-48695	Sequence 48695, A	1106	119	3.8	809	7	US-10-505-928-150	Sequence 150, App
1034	120.5	3.8	1052	6	US-10-535-573-170	Sequence 170, App	1107	118.5	3.8	5738	6	US-10-953-349-20505	Sequence 20505, A
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1036	120.5	3.8	1618	7	US-11-375-615-46	Sequence 46, Appl	1109	118.5	3.8	373	7	US-11-056-355B-62373	Sequence 62373, A
1037	120.5	3.8	294	7	US-11-051-725-80	Sequence 80, Appl	1110	118.5	3.8	400	6	US-10-528-948-12	Sequence 12, Appl
1038	120.5	3.8	294	7	US-11-051-725-82	Sequence 82, Appl	1111	118.5	3.8	400	6	US-10-528-948-4	Sequence 4, Appl
1039	120.5	3.8	294	7	US-11-051-725-88	Sequence 88, Appl	1112	118.5	3.8	400	6	US-10-528-948-6	Sequence 6, Appl
1040	120	3.8	294	7	US-11-051-725-98	Sequence 98, Appl	1113	118.5	3.8	400	6	US-10-528-948-8	Sequence 8, Appl
1041	120	3.8	292	7	US-10-449-902-32733	Sequence 32733, A	1114	118.5	3.8	400	6	US-10-528-948-10	Sequence 10, Appl
1042	120	3.8	332	6	US-10-449-902-54788	Sequence 54788, A	1115	118.5	3.8	400	6	US-10-528-948-14	Sequence 14, Appl
1043	120	3.8	332	6	US-10-449-902-54788	Sequence 54788, A	1116	118.5	3.8	400	6	US-11-371-354-58085	Sequence 58085, A
1044	120	3.8	373	6	US-10-953-349-31149	Sequence 31149, A	1117	118.5	3.8	431	7	US-11-520-715-68108	Sequence 68108, A
1045	120	3.8	472	7	US-11-520-715-64662	Sequence 64662, A	1118	118.5	3.8	431	7	US-10-538-002-136	Sequence 136, App
1046	120	3.8	546	7	US-11-056-355B-19161	Sequence 19161, A	1119	118.5	3.8	469	6	US-11-056-355B-91071	Sequence 91071, A
1047	120	3.8	560	6	US-10-449-902-53097	Sequence 53097, A	1120	118.5	3.8	998	7	US-11-056-355B-94827	Sequence 94827, A
1048	120	3.8	569	7	US-11-262-514-22	Sequence 22, Appl	1121	118.5	3.8	998	7	US-11-056-355B-94826	Sequence 94826, A
1049	120	3.8	569	7	US-11-317-260-22	Sequence 22, Appl	1122	118.5	3.8	1010	7	US-11-056-355B-91070	Sequence 91070, A
1050	120	3.8	651	6	US-10-533-519-58	Sequence 58, Appl	1123	118.5	3.8	1010	7	US-11-056-355B-94826	Sequence 94826, A
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1052	120	3.8	892	6	US-10-977-350-4	Sequence 4, Appl	1125	118	3.8	262	6	US-11-056-355B-63081	Sequence 63081, A
1053	120	3.8	892	6	US-11-330-500-9	Sequence 9, Appl	1126	118	3.8	266	7	US-11-426-236-7	Sequence 7, Appl
1054	120	3.8	1047	6	US-10-449-902-53278	Sequence 53278, A	1127	118	3.8	266	7	US-11-426-279-7	Sequence 7, Appl
1055	120	3.8	2556	6	US-10-781-059A-2	Sequence 2, Appl	1128	118	3.8	266	7	US-11-426-286-7	Sequence 7, Appl
1056	119.5	3.8	254	7	US-11-520-715-70408	Sequence 70408, A	1129	118	3.8	266	7	US-11-056-355B-7182	Sequence 7182, Ap
1057	119.5	3.8	322	7	US-11-520-715-61309	Sequence 61309, A	1130	118	3.8	438	7	US-11-056-355B-65494	Sequence 65494, A
1058	119.5	3.8	383	6	US-10-449-902-43496	Sequence 43496, A	1131	118	3.8	493	7	US-11-056-355B-46949	Sequence 46949, A
1059	119.5	3.8	667	7	US-11-520-715-65119	Sequence 65119, A	1132	118	3.8	1000	7	US-11-056-355B-46948	Sequence 46948, A
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1062	119.5	3.8	941	6	US-11-056-355B-72901	Sequence 72901, A	1135	118	3.8	1033	6	US-11-265-762-114	Sequence 114, App
1063	119.5	3.8	1031	6	US-10-449-902-52986	Sequence 52986, A	1136	118	3.8	1050	6	US-10-449-902-41453	Sequence 41453, A
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1066	119.5	3.8	1104	7	US-11-056-355B-117672	Sequence 117672, A	1139	118	3.8	2471	6	US-10-781-059A-1	Sequence 1, Appl
1067	119.5	3.8	1106	7	US-11-056-355B-106432	Sequence 106432, A	1140	118	3.8	2471	6	US-10-219-051B-4114	Sequence 4114, Ap
1068	119.5	3.8	1106	7	US-11-056-355B-117671	Sequence 117671, A	1141	118	3.8	2471	6	US-10-219-051B-4116	Sequence 4116, Ap
1069	119.5	3.8	1128	7	US-11-056-355B-106431	Sequence 106431, A	1142	118	3.8	2471	6	US-10-219-051B-9647	Sequence 9647, Ap
1070	119.5	3.8	1128	7	US-11-056-355B-117670	Sequence 117670, A	1143	118	3.8	2471	6	US-10-219-051B-9651	Sequence 9651, Ap
1071	119.5	3.8	1597	7	US-11-407-702-78	Sequence 78, Appl	1144	118	3.8	2471	6	US-10-219-051B-9655	Sequence 9655, Ap
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1073	119	3.8	286	7	US-11-520-715-55260	Sequence 55260, A	1146	118	3.8	2471	6	US-11-071-796A-23	Sequence 23, Appl
1074	119	3.8	290	7	US-11-520-715-67727	Sequence 67727, A	1147	117.5	3.7	369	6	US-10-449-902-50707	Sequence 50707, A
1075	119	3.8	309	7	US-11-520-715-41158	Sequence 41158, A	1148	117.5	3.7	413	7	US-11-056-355B-4735	Sequence 4735, Ap
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1078	119	3.8	383	7	US-11-090-997-1040	Sequence 1040, Ap	1151	117.5	3.7	550	7	US-11-056-355B-75616	Sequence 75616, A
1079	119	3.8	406	6	US-10-449-902-42711	Sequence 42711, A	1152	117.5	3.7	550	7	US-11-056-355B-96078	Sequence 96078, A
1080	119	3.8	554	6	US-10-449-902-46816	Sequence 46816, A	1153	117.5	3.7	555	6	US-10-484-603-1	Sequence 1, Appl
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1085	119	3.8	627	7	US-11-330-403-544	Sequence 544, App	1158	117.5	3.7	745	7	US-11-520-715-70991	Sequence 70991, A

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1165	117.5	3.7	870	6	US-10-539-228-358	Sequence 358, Appl	1238	115.5	3.7	911	7	US-11-248-718-89	Sequence 89, Appl
1166	117.5	3.7	3664	6	US-10-574-398-79	Sequence 79, Appl	1239	115.5	3.7	911	7	US-11-036-255A-8	Sequence 8, Appl
1167	117	3.7	215	6	US-10-612-783-3768	Sequence 3768, Ap	1240	115.5	3.7	911	7	US-11-371-354-55327	Sequence 55327, A
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1170	117	3.7	649	7	US-11-520-715-48673	Sequence 48673, A	1243	115.5	3.7	1450	7	US-11-217-997-6	Sequence 6, Appl
1171	117	3.7	655	7	US-11-242-617-1	Sequence 1, Appl	1244	115.5	3.7	3515	6	US-10-526-572-12	Sequence 12, Appl
1172	117	3.7	677	7	US-11-520-715-55399	Sequence 55399, A	1245	115	3.7	227	6	US-10-953-349-32122	Sequence 32122, A
1173	117	3.7	681	6	US-10-953-349-10919	Sequence 10919, A	1246	115	3.7	337	7	US-11-174-307B-4220	Sequence 4220, Ap
1174	117	3.7	681	7	US-11-056-355B-45477	Sequence 45477, A	1247	115	3.7	417	6	US-10-526-572-31	Sequence 31, Appl
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1176	117	3.7	698	6	US-10-449-902-53993	Sequence 53993, A	1249	115	3.7	468	7	US-11-371-354-13758	Sequence 13758, A
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1184	117	3.7	1238	7	US-11-178-724-22	Sequence 22, Appl	1257	115	3.7	717	7	US-11-166-372-2120	Sequence 2120, Ap
1185	117	3.7	1238	7	US-11-071-796A-21	Sequence 21, Appl	1258	115	3.7	740	6	US-10-449-902-51311	Sequence 51311, A
1186	117	3.7	1238	7	US-11-188-417A-22	Sequence 22, Appl	1259	115	3.7	756	7	US-11-056-355B-89081	Sequence 89081, A
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1188	117	3.7	1463	7	US-11-288-992-48	Sequence 48, Appl	1261	115	3.7	757	7	US-11-056-355B-50711	Sequence 50711, A
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1192	116.5	3.7	184	7	US-11-056-355B-30244	Sequence 30244, A	1265	115	3.7	1218	6	US-10-833-833-121	Sequence 121, App
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1195	116.5	3.7	517	7	US-11-520-715-70798	Sequence 70798, A	1268	115	3.7	1375	6	US-10-553-436-181	Sequence 181, App
1196	116.5	3.7	573	7	US-11-520-715-52798	Sequence 52798, A	1269	114.5	3.7	269	7	US-11-520-715-38093	Sequence 38093, A
1197	116.5	3.7	677	7	US-11-520-715-70127	Sequence 70127, A	1270	114.5	3.7	297	6	US-10-953-349-31196	Sequence 31196, A
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1203	116.5	3.7	1460	7	US-11-030-997-1414	Sequence 1414, Ap	1276	114.5	3.7	373	7	US-11-056-355B-41941	Sequence 41941, A
1204	116.5	3.7	2837	6	US-10-526-572-13	Sequence 13, Appl	1277	114.5	3.7	376	7	US-11-520-715-51014	Sequence 51014, A
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1206	116	3.7	321	6	US-10-540-845-5	Sequence 5, Appl	1279	114.5	3.7	411	6	US-11-056-355B-66649	Sequence 66649, A
1207	116	3.7	363	6	US-10-540-845-17	Sequence 17, Appl	1280	114.5	3.7	412	6	US-10-953-349-31855	Sequence 31855, A
1208	116	3.7	377	6	US-10-953-349-9913	Sequence 9913, Ap	1281	114.5	3.7	412	6	US-11-056-355B-66648	Sequence 66648, A
1209	116	3.7	383	6	US-10-540-845-16	Sequence 16, Appl	1282	114.5	3.7	435	6	US-10-449-902-42063	Sequence 42063, A
1210	116	3.7	383	7	US-11-166-372-2006	Sequence 2006, Ap	1283	114.5	3.7	451	6	US-10-953-349-31854	Sequence 31854, A
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1213	116	3.7	430	7	US-11-520-715-52528	Sequence 52528, A	1286	114.5	3.7	506	7	US-11-371-354-64247	Sequence 64247, A
1214	116	3.7	431	7	US-11-371-354-57067	Sequence 57067, A	1287	114.5	3.7	514	7	US-11-520-715-55766	Sequence 55766, A
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1216	116	3.7	474	6	US-10-953-349-9911	Sequence 9911, Ap	1289	114.5	3.7	647	7	US-11-371-354-61789	Sequence 61789, A
1217	116	3.7	673	6	US-10-449-902-54133	Sequence 54133, A	1290	114.5	3.7	688	7	US-11-330-403-5573	Sequence 5573, Ap
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1219	116	3.7	902	7	US-11-413-976-8	Sequence 8, Appl	1292	114.5	3.7	894	7	US-11-389-343-1099	Sequence 1099, Ap
1220	116	3.7	1014	6	US-10-449-902-52994	Sequence 52994, A	1293	114.5	3.7	894	7	US-11-389-343-1116	Sequence 1116, Ap
1221	116	3.7	1181	7	US-11-404-939-587	Sequence 587, App	1294	114.5	3.7	894	7	US-11-389-343-1117	Sequence 1117, Ap
1222	116	3.7	1291	6	US-10-532-740-6	Sequence 6, Appl	1295	114.5	3.7	894	7	US-11-389-017-1099	Sequence 1099, Ap
1223	116	3.7	1953	6	US-11-284-443-16	Sequence 16, Appl	1296	114.5	3.7	894	7	US-11-389-017-1116	Sequence 1116, Ap
1224	116	3.7	2505	6	US-10-669-920-15	Sequence 15, Appl	1297	114.5	3.7	894	7	US-11-389-017-1117	Sequence 1117, Ap
1225	116	3.7	2556	7	US-11-071-796A-22	Sequence 22, Appl	1298	114.5	3.7	910	7	US-11-056-355B-79291	Sequence 79291, A
1226	116	3.7	3934	7	US-11-165-586-20	Sequence 20, Appl	1299	114.5	3.7	970	7	US-11-056-355B-79290	Sequence 79290, A
1227	115.5	3.7	361	7	US-11-357-421-316	Sequence 316, App	1300	114.5	3.7	1046	7	US-11-056-355B-79289	Sequence 79289, A
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1230	115.5	3.7	396	7	US-11-056-355B-83842	Sequence 83842, A	1303	114.5	3.7	1139	6	US-10-449-902-52733	Sequence 52733, A
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1232	115.5	3.7	690	7	US-11-520-715-49019	Sequence 49019, A	1305	114.5	3.7	1218	6	US-10-833-833-124	Sequence 124, App
1233	115.5	3.7	822	7	US-11-056-355B-96337	Sequence 96337, A	1306	114.5	3.7	1218	6	US-10-219-051B-6286	Sequence 6286, Ap
1234	115.5	3.7	849	7	US-11-056-355B-79057	Sequence 79057, A	1307	114.5	3.7	1218	7	US-11-178-724-21	Sequence 21, Appl
1235	115.5	3.7	856	6	US-10-449-902-41385	Sequence 41385, A	1308	114.5	3.7	1218	7	US-11-071-796A-20	Sequence 20, Appl
1236	115.5	3.7	911	6	US-10-219-051B-8514	Sequence 8514, Ap	1309	114.5	3.7	1218	7	US-11-188-417A-21	Sequence 21, Appl

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1482	112	3.6	764	7	US-11-188-417A-92	Sequence 92, Appl
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1484	112	3.6	864	7	US-11-178-724-27	Sequence 27, Appl
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1486	112	3.6	864	7	US-11-231-494-34	Sequence 34, Appl
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3	1213.5	38.7	661	1 VASN XENTR	Q6df55 xenopus tro
4	972.5	31.0	688	2 Q3MK9 BRARE	Q3mk9 brachydanio
5	927.5	29.6	643	2 Q5032 BRARE	Q5032 brachydanio
6	914.5	29.2	962	2 Q4SQ8 TETNG	Q4sq8 tetradon n
7	368.5	11.8	513	1 LRC24 HUMAN	Q50199 homo sapien
8	359.5	11.5	635	1 LRFN4 MOUSE	Q80x8 mus musculu
9	351	11.2	636	1 LRFN4 MOUSE	Q460G5 mus musculu
10	348	11.1	636	2 Q3UV6 MOUSE	Q3uv6 mus musculu
11	341	10.9	634	2 Q3BLUO MOUSE	Q3bluo m adult mal
12	341	10.9	660	2 Q8L24 MOUSE	Q8l24 mus musculu
13	339	10.8	521	1 LRC24 MOUSE	Q8sgv9 tetradon n
14	338	10.8	655	2 Q4SGV9 TETNG	Q4sgv9 tetradon n
15	332	10.6	637	2 Q6A073 MOUSE	Q6a073 mus musculu
16	331.5	10.6	622	2 Q59GV4 HUMAN	Q59gv4 homo sapien
17	330	10.5	653	1 LRC4 HUMAN	Q8hbw1 homo sapien
18	329.5	10.5	648	2 Q6DDY0 XENLA	Q6ddy0 xenopus lae
19	325.5	10.4	570	2 Q70AK2 XENLA	Q70ak2 xenopus lae
20	324	10.3	626	1 LRFN3 MOUSE	Q8bly3 mus musculu
21	324	10.3	626	2 Q50582 MOUSE	Q50582 mus musculu
22	323	10.3	732	2 Q4RPB8 TETNG	Q4rpb8 tetradon n
23	322.5	10.3	682	2 Q6DJ2 XENLA	Q6dj2 xenopus lae
24	322.5	10.3	811	2 Q7L0X0 HUMAN	Q7l0x0 homo sapien
25	322.5	10.3	887	2 Q5139 HUMAN	Q5139 homo sapien
26	322	10.3	605	1 ALS PAPH	Q02833 papio hamad
27	321.5	10.3	709	1 LRFN3 MOUSE	P0c192 mus musculu
28	321	10.2	628	1 LRFN3 HUMAN	Q9bnt0 homo sapien
29	321	10.2	762	2 Q5JY13 HUMAN	Q5jy13 homo sapien
30	320.5	10.2	597	2 Q3I0Y3 BOVIN	Q3i0y3 bos taurus
31	320	10.2	660	1 FLRT2 HUMAN	Q43155 homo sapien

32	320	10.2	674	2 Q6RKD8 MOUSE	Q6rk8 m fibronect
33	319	10.2	602	2 Q58CS0 BOVIN	Q58cs0 bos taurus
34	319	10.2	652	2 Q45R42 RAT	Q45r42 rattus norv
35	318.5	10.2	652	1 LRRCA4 MOUSE	Q99ph1 mus musculu
36	317	10.1	778	2 Q6NUI6 HUMAN	Q6nui6 homo sapien
37	316.5	10.1	713	1 LRC4B HUMAN	Q9nt99 homo sapien
38	313	10.0	628	2 Q1RMS4 BOVIN	Q1rme4 bos taurus
39	312.5	10.0	648	2 Q70AK3 XENLA	Q70ak3 xenopus lae
40	312.5	10.0	935	2 Q4SBT7 TETNG	Q4sb7 tetradon n
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42	310.5	9.9	420	1 R4RL2 RAT	Q80wd1 rattus norv
43	310.5	9.9	646	1 FLRT1 HUMAN	Q80wd1 rattus norv
44	308	9.8	627	2 Q8NC95 HUMAN	Q8nc95 homo sapien
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48	307.5	9.8	674	2 Q8WVA2 HUMAN	Q8wva2 homo sapien
49	307	9.8	637	2 Q68P21 XENLA	Q68p21 xenopus lae
50	307	9.8	649	2 Q5R6T0 PONPY	Q5r6t0 pongo pygma
51	306.5	9.8	730	2 Q6P6P6 MOUSE	Q6p6p6 mus musculu
52	305.5	9.7	730	2 Q6US92 MOUSE	Q6us92 mus musculu
53	303.5	9.7	692	2 Q4G0S0 HUMAN	Q4g0s0 homo sapien
54	302.5	9.6	420	1 R4RL2 HUMAN	Q86un3 homo sapien
55	302.5	9.6	420	2 Q17RL3 HUMAN	Q17rl3 homo sapien
56	302.5	9.6	618	2 Q4SHD7 TETNG	Q4shd7 tetradon n
57	302	9.6	605	1 ALS HUMAN	P35858 homo sapien
58	302	9.6	605	2 Q8TAY0 HUMAN	Q8tay0 homo sapien
59	299.5	9.6	677	2 Q28256 CANFA	Q28256 canis famil
60	298.5	9.5	649	2 Q8BGT1 MOUSE	Q8bgt1 m 12 days e
61	298.5	9.5	663	2 Q6ZP01 MOUSE	Q6zpq1 mus musculu
62	295.5	9.4	640	1 NGL1 MOUSE	Q8c031 mus musculu
63	295.5	9.4	640	2 Q50SE5 MOUSE	Q50se5 mus musculu
64	294.5	9.4	647	2 Q50317 BRARE	Q50317 brachydanio
65	293.5	9.4	372	2 Q499C1 BRARE	Q499c1 brachydanio
66	293.5	9.4	809	2 Q9DBY4 MOUSE	Q9db4 m adult mal
67	292.5	9.3	640	1 NGL1 HUMAN	Q9hcl2 homo sapien
68	292.5	9.3	811	2 Q496Z2 RAT	Q496z2 rattus norv
69	292.5	9.3	837	2 Q80TV0 MOUSE	Q80tv0 mus musculu
70	288.5	9.2	372	2 Q7T2W3 BRARE	Q7t2w3 brachydanio
71	288.5	9.2	581	2 Q4SY17 TETNG	Q4sy17 tetradon n
72	288.5	9.2	640	2 Q4JIW0 HUMAN	Q4jiw0 homo sapien
73	287.5	9.2	428	2 Q4S4W6 TETNG	Q4s4w6 tetradon n
74	287.5	9.2	713	1 LRRN5 HUMAN	Q75325 homo sapien
75	286	9.1	650	2 Q4RQ15 TETNG	Q4rq15 tetradon n
76	285	9.1	640	2 Q4JIV9 HUMAN	Q4jiv9 homo sapien
77	284.5	9.1	457	2 Q6WZD1 BRARE	Q6wzd1 brachydanio
78	284	9.1	782	2 Q5TOV4 HUMAN	Q5tov4 homo sapien
79	283.5	9.0	603	2 Q70211 RAT	Q70211 rattus norv
80	283	9.0	1515	2 Q9DE37 BRARE	Q9de37 brachydanio
81	282.5	9.0	745	2 Q6UXK2 HUMAN	Q6uxk2 homo sapien
82	282.5	9.0	785	2 Q9P263 HUMAN	Q9p263 homo sapien
83	282	9.0	626	1 GP1BA HUMAN	P07359 homo sapien
84	281.5	9.0	603	1 ALS RAT	P35859 rattus norv
85	281	9.0	738	2 Q90Z45 CHICK	Q90z45 gallus gall
86	280	8.9	633	2 Q4SR95 TETNG	Q4sr95 tetradon n
87	279.5	8.9	331	2 Q4YDZ4 EPTST	Q4ydz4 eptatretus
88	279.5	8.9	619	2 Q570Z9 MOUSE	Q570z9 mus musculu
89	278.5	8.9	301	2 Q3KQP3 MOUSE	Q3kqp3 mus musculu
90	278.5	8.9	603	1 ALS MOUSE	P70389 mus musculu
91	278.5	8.9	603	2 Q79I05 MOUSE	Q79i05 mus musculu
92	278.5	8.9	687	2 Q9JIL0 MOUSE	Q9jil0 mus musculu
93	278	8.9	321	2 Q6E4K4 PETMA	Q6e4k4 petromyzon
94	278	8.9	1531	1 SLIT1 RAT	Q88279 rattus norv
95	277	8.8	330	2 Q4G1K9 EPTBU	Q4g1k9 eptatretus
96	277	8.8	1532	2 Q3Y6S4 BRARE	Q3y6s4 brachydanio
97	276.5	8.8	347	2 Q32Q8 EPTST	Q32q8 eptatretus
98	276	8.8	1071	2 Q4RT16 TETNG	Q4rt16 tetradon n
99	276	8.8	1531	1 SLIT1 MOUSE	Q80tr4 mus musculu
100	276	8.8	2623	2 Q6WR10 HUMAN	Q6wr10 homo sapien
101	275	8.8	358	2 Q2YEO1 EPTST	Q2ye01 eptatretus
102	273.5	8.7	593	2 Q6UY18 HUMAN	Q6uy18 homo sapien
103	273.5	8.7	1504	1 SLIT DRONE	P24014 drosophila
104	273	8.7	745	2 Q5RKR3 MOUSE	Q5rkr3 mus musculu

105	Q6ZPQ3_MOUSE	273	8.7	785	2	Q6ZPQ3_MOUSE	178	251	8.0	1021	2	Q9V430_DROME	Q9v430 drosophila
106	Q3S2J2_BRARE	272.5	8.7	1524	2	Q3S2J2_BRARE	179	250	8.0	412	2	Q4RRU8_TETNG	Q4rru8 tetraodon n
107	Q32Q02_EPTST	272	8.7	372	2	Q32Q02_EPTST	180	249.5	8.0	412	2	Q32Q01_EPTST	Q32qq1 eptatretus
108	Q91XU1_MOUSE	271.5	8.7	342	2	Q91XU1_MOUSE	181	249.5	8.0	789	1	LRFN2_HUMAN	Q9ulh4 homo sapien
109	Q32Q06_EPTST	271.5	8.7	347	2	Q32Q06_EPTST	182	249.5	8.0	789	1	LRFN2_MACFA	Q9be12 macaca fasc
110	Q61PFO_CAEBR	271.5	8.7	1312	2	Q61PFO_CAEBR	183	249.5	8.0	2597	2	Q6WRH9_RAT	Q6wrh9 rattus norv
111	Q32Q05_EPTST	271	8.6	372	2	Q32Q05_EPTST	184	248.5	7.9	420	1	TPBG_MACFA	Q4r8y9 macaca fasc
112	RTN4R_HUMAN	271	8.6	473	1	RTN4R_HUMAN	185	248	7.9	284	2	Q2YE15_EPTST	Q2ye15 eptatretus
113	RTN4R_MACFA	271	8.6	473	1	RTN4R_MACFA	186	248	7.9	481	1	NYX_HUMAN	Q9gzus homo sapien
114	Q6PK41_HUMAN	270.5	8.6	541	2	Q6PK41_HUMAN	187	248	7.9	481	1	Q2MIS4_HUMAN	Q2mls4 homo sapien
115	Q6WZD2_BRARE	270	8.6	478	2	Q6WZD2_BRARE	188	247.5	7.9	305	2	Q4GLI3_EPTBU	Q4gli3 eptatretus
116	Q5VM18_HUMAN	270	8.6	1461	2	Q5VM18_HUMAN	189	247.5	7.9	323	2	Q32Q17_EPTST	Q32q17 eptatretus
117	SLIT1_HUMAN	270	8.6	1534	1	SLIT1_HUMAN	190	247.5	7.9	323	2	Q32QX2_EPTST	Q32qx2 eptatretus
118	Q5VM17_HUMAN	270	8.6	1534	2	Q5VM17_HUMAN	191	247.5	7.9	739	2	Q2PNW3_XENLA	Q2pnw3 xenopus lae
119	Q5T0V2_HUMAN	268.5	8.5	409	2	Q5T0V2_HUMAN	192	247.5	7.9	1521	1	SLIT2_MOUSE	Q9r1b9 mus musculus
120	Q6E4U7_PETWA	268	8.5	417	2	Q6E4U7_PETWA	193	247.5	7.9	1529	1	SLIT2_HUMAN	Q94813 homo sapien
121	Q9DE36_BRARE	267.5	8.5	1512	2	Q9DE36_BRARE	194	247.5	7.9	1529	1	Q17RU3_HUMAN	Q17ru3 homo sapien
122	Q7ZX12_XENLA	266.5	8.5	1529	2	Q7ZX12_XENLA	195	247.5	7.9	1530	2	Q90WZ3_XENLA	Q90wz3 xenopus lae
123	Q61P16_HUMAN	266	8.5	460	2	Q61P16_HUMAN	196	247	7.9	794	2	Q4SK16_TETNG	Q4sk16 tetraodon n
124	Q35930_MOUSE	266	8.5	734	2	Q35930_MOUSE	197	247	7.9	1473	2	Q28WZ1_DROPS	Q28wz1 drosophila
125	Q5ISR9_MACFA	265.5	8.5	1044	2	Q5ISR9_MACFA	198	246.5	7.9	283	2	Q2YE14_EPTST	Q2ye14 eptatretus
126	Q4GLI7_PETBU	265	8.5	298	2	Q4GLI7_PETBU	199	246.5	7.9	323	2	Q2YE02_EPTST	Q2ye02 eptatretus
127	Q5SX47_MOUSE	265	8.5	734	2	Q5SX47_MOUSE	200	246.5	7.9	371	2	Q32Q06_EPTST	Q32qp6 eptatretus
128	TPBG_HUMAN	264.5	8.4	420	1	TPBG_HUMAN	201	246	7.8	264	2	Q2VGV6_PETWA	Q2vgy6 petromyzon
129	Q2I0M4_HUMAN	264	8.4	334	2	Q2I0M4_HUMAN	202	246	7.8	306	2	Q2YE10_EPTST	Q2ye10 eptatretus
130	Q5VSG2_HUMAN	264	8.4	334	2	Q5VSG2_HUMAN	203	246	7.8	308	2	Q4GLI3_EPTST	Q4gli3 eptatretus
131	Q4GLI1_PETBU	264	8.4	352	2	Q4GLI1_PETBU	204	246	7.8	346	2	Q2KIF2_BOVIN	Q2kif2 bos taurus
132	Q2YD25_EPTST	263	8.4	308	2	Q2YD25_EPTST	205	245.5	7.8	331	2	Q3UUY1_MOUSE	Q3uuy1 m 6 days ne
133	Q5I0B1_RAT	263	8.4	332	2	Q5I0B1_RAT	206	245.5	7.8	331	2	Q91W20_MOUSE	Q91w20 m cda sequ
134	Q4T0S1_TETNG	263	8.4	1253	2	Q4T0S1_TETNG	207	245.5	7.8	346	2	Q32QY6_EPTBU	Q32qy6 eptatretus
135	Q16WM1_AEDAE	262.5	8.4	1393	2	Q16WM1_AEDAE	208	245.5	7.8	544	2	Q61X58_CAEBR	Q61x58 caenorhabdi
136	Q4GLI9_PETBU	262	8.4	345	2	Q4GLI9_PETBU	209	245.5	7.8	788	2	Q460M5_RAT	Q460m5 rattus norv
137	R2GL_HUMAN	261.5	8.3	347	1	R2GL_HUMAN	210	245	7.8	306	2	Q4G1K6_EPTST	Q4g1k6 eptatretus
138	Q2YE28_EPTBU	261	8.3	318	2	Q2YE28_EPTBU	211	245	7.8	321	2	Q6E4J9_PETWA	Q6e4j9 petromyzon
139	Q2YE06_EPTST	261	8.3	341	2	Q2YE06_EPTST	212	245	7.8	708	1	LRRN3_PONPY	Q6r492 pongo pygma
140	SLIT3_RAT	261	8.3	1523	1	SLIT3_RAT	213	244.5	7.8	411	2	Q4S6L6_TETNG	Q4s6l6 tetraodon n
141	Q2YE31_EPTST	260	8.3	306	2	Q2YE31_EPTST	214	244.5	7.8	718	2	Q73675_XENLA	Q73675 xenopus lae
142	Q2YE78_EPTST	259	8.3	370	2	Q2YE78_EPTST	215	244.5	7.8	766	1	LRFN2_MOUSE	Q80t99 mus musculus
143	Q6E4D1_PETMA	258	8.2	321	2	Q6E4D1_PETMA	216	244.5	7.8	788	1	LRFN2_MOUSE	Q80t99 mus musculus
144	Q2YE77_EPTST	258	8.2	370	2	Q2YE77_EPTST	217	244.5	7.8	1593	2	Q5DYL5_MOUSE	Q5dtl5 mus musculus
145	Q2YE77_EPTST	258	8.2	370	2	Q2YE77_EPTST	218	244	7.8	346	2	Q32QV4_EPTST	Q32qv4 eptatretus
146	Q4S3K9_TETNG	257.5	8.2	324	2	Q4S3K9_TETNG	219	244	7.8	458	2	Q6WZD3_BRARE	Q6wzd3 brachydanio
147	Q32QX0_EPTST	257.5	8.2	347	2	Q32QX0_EPTST	220	244	7.8	567	1	LRRN3_HUMAN	Q9h3w5 homo sapien
148	Q4SZC5_TETNG	257.5	8.2	501	2	Q4SZC5_TETNG	221	244	7.8	708	1	Q32QR8_EPTST	Q32qr8 eptatretus
149	Q2YD26_EPTST	257	8.2	306	2	Q2YD26_EPTST	222	243.5	7.8	347	2	Q32Q08_EPTST	Q32q08 eptatretus
150	RTN4R_RAT	257	8.2	473	1	RTN4R_RAT	223	243.5	7.8	476	1	NYX_MOUSE	P83503 mus musculus
151	Q8BRK5_MOUSE	257	8.2	739	2	Q8BRK5_MOUSE	224	243	7.8	242	2	Q2VGK4_PETWA	Q2vgy4 petromyzon
152	Q4SGG5_TETNG	256.5	8.2	342	2	Q4SGG5_TETNG	225	243	7.8	290	2	Q2VGK3_PETWA	Q2vgy3 petromyzon
153	Q90XG4_CHICK	255.5	8.1	1095	2	Q90XG4_CHICK	226	243	7.8	321	2	Q6E4L4_PETWA	Q6e4l4 petromyzon
154	Q3V1M1_MOUSE	254.5	8.1	1196	2	Q3V1M1_MOUSE	227	243	7.8	323	2	Q32QV0_EPTST	Q32qv0 eptatretus
155	Q8N644_HUMAN	254	8.1	528	2	Q8N644_HUMAN	228	242.5	7.7	355	2	Q2YE75_EPTST	Q2ye75 eptatretus
156	SLIT3_MOUSE	254	8.1	1523	1	SLIT3_MOUSE	229	242.5	7.7	371	2	Q32QW7_EPTST	Q32qw7 eptatretus
157	Q3UHN1_MOUSE	254	8.1	1523	2	Q3UHN1_MOUSE	230	242.5	7.7	388	2	Q6KFI2_LAMAP	Q6kfi2 lampetra ap
158	Q5SS56_MOUSE	254	8.1	1523	2	Q5SS56_MOUSE	231	242.5	7.7	545	1	Q4E4L3_PETWA	Q4e4l3 petromyzon
159	Q68CK4_HUMAN	253.5	8.1	347	2	Q68CK4_HUMAN	232	242.5	7.7	718	2	Q2VGH4_PETWA	Q2vgh4 petromyzon
160	Q3UPM4_MOUSE	253.5	8.1	429	2	Q3UPM4_MOUSE	233	242	7.7	220	2	Q2VGF4_PETWA	Q2vgh4 petromyzon
161	Q6GQU6_MOUSE	253.5	8.1	589	2	Q6GQU6_MOUSE	234	242	7.7	266	2	Q5T0V3_HUMAN	Q5t0v3 homo sapien
162	Q20204_CABEL	253.5	8.1	1410	2	Q20204_CABEL	235	242	7.7	380	2	Q7FVZ3_ANOGA	Q7fpv23 anopheles g
163	Q32Q03_EPTST	253	8.1	368	2	Q32Q03_EPTST	236	241.5	7.7	272	2	Q4KFI2_LAMAP	Q4kfi2 lampetra ap
164	TPBG_MOUSE	253	8.1	426	1	TPBG_MOUSE	237	241.5	7.7	311	2	Q6E4L3_PETWA	Q6e4l3 petromyzon
165	Q3UP12_MOUSE	253	8.1	426	2	Q3UP12_MOUSE	238	241	7.7	330	2	Q2YD29_EPTST	Q2ydz9 eptatretus
166	GPV_MOUSE	253	8.1	567	1	GPV_MOUSE	239	241	7.7	299	2	Q2YD23_EPTST	Q2ydz3 eptatretus
167	Q2YE08_EPTST	252.5	8.1	323	2	Q2YE08_EPTST	240	240.5	7.7	323	2	Q32QY1_EPTST	Q32qy1 eptatretus
168	Q6E4U1_PETMA	252	8.0	311	2	Q6E4U1_PETMA	241	240.5	7.7	323	2	Q2YB62_EPTST	Q2ybe2 eptatretus
169	TPBG_RAT	252	8.0	426	1	TPBG_RAT	242	240.5	7.7	323	2	Q32QX5_EPTST	Q32qx5 eptatretus
170	Q3TA66_MOUSE	252	8.0	567	2	Q3TA66_MOUSE	243	240.5	7.7	323	2	Q2YD22_EPTST	Q2ydz2 eptatretus
171	Q9QZU3_MOUSE	252	8.0	567	2	Q9QZU3_MOUSE	244	240	7.7	308	2	Q2YD22_EPTST	Q2ydz2 eptatretus
172	Q2YD28_EPTST	251.5	8.0	309	2	Q2YD28_EPTST	245	240	7.7	560	1	GPV_HUMAN	P40197 homo sapien
173	RTN4R_MOUSE	251	8.0	473	1	RTN4R_MOUSE	246	239.5	7.6	307	2	Q2YE04_EPTST	Q2ye04 eptatretus
174	Q9N4G6_CABEL	251	8.0	542	2	Q9N4G6_CABEL	247	239.5	7.6	370	2	Q8BGX3_MOUSE	Q8bgx3 m adult mal
175	Q1KS52_PIG	251	8.0	606	2	Q1KS52_PIG	248	239.5	7.6	786	2	Q5TU01_ANOGA	Q5tu01 anopheles g
176	Q7Z207_HUMAN	251	8.0	622	2	Q7Z207_HUMAN	249	239.5	7.6	1256	2	Q7QCT2_ANOGA	Q7qct2 anopheles g
177	Q6ZW15_HUMAN	251	8.0	622	2	Q6ZW15_HUMAN	250	238.5	7.6	347	2	Q2YE56_EPTST	Q2ye56 eptatretus

251	238.5	7.6	995	2	Q29KV3	DROPS	Q29kv3	drosophila	324	228	7.3	310	2	Q4RRQ4	TETNG	Q4rrq4	tetraodon n
252	238	7.6	323	2	Q4KP13	9PETR	Q4kp13	ichthyomyzo	325	228	7.3	322	2	Q32QP0	EPTST	Q32qp0	eptaretus n
253	238	7.6	348	2	Q2YE73	EPTST	Q2ye73	eptaretus	326	228	7.3	838	2	Q4SPP9	TETNG	Q4spp9	tetraodon n
254	238	7.6	453	2	Q86XY1	HUMAN	Q86xy1	homo sapien	327	227.5	7.3	356	2	Q8BXQ3	MOUSE	Q8bxq3	m adult ret
255	238	7.6	544	2	Q8UV23	9PERC	Q8uv23	sphoeroides	328	227	7.2	311	1	LRC55	MOUSE	Q8uy51	mus musculus
256	237.5	7.6	346	2	Q2YE74	EPTST	Q2ye74	eptaretus	329	227	7.2	311	1	LRC55	RAT	Q4kl13	rattus norv
257	237.5	7.6	346	2	Q32R39	EPTBU	Q32r39	eptaretus	330	227	7.2	321	2	Q32R27	EPTBU	Q32r27	eptaretus
258	237.5	7.6	391	2	Q9D3X0	MOUSE	Q9d3x0	m 6 days ne	331	227	7.2	321	2	Q2YE58	EPTST	Q2ye58	eptaretus
259	237.5	7.6	1174	2	Q4S4C0	TETNG	Q4s4c0	tetraodon n	332	227	7.2	371	2	Q32R26	EPTBU	Q32r26	eptaretus
260	237	7.6	289	2	Q4KP06	LAMAP	Q4kp06	lampetra ap	333	227	7.2	783	2	Q90XG2	CHICK	Q90xg2	gallus gall
261	237	7.6	370	2	Q8N967	HUMAN	Q8n967	homo sapien	334	227	7.2	950	2	Q90Z44	CHICK	Q90z44	gallus gall
262	237	7.6	578	1	LRC15	RAT	Q8r5m3	rattus norv	335	226.5	7.2	209	2	Q2VGN5	PETWA	Q2vgn5	petromyzon
263	237	7.6	707	1	LRRN3	RAT	Q8esv6	rattus norv	336	226.5	7.2	283	2	Q4GI11	EPTST	Q4gi11	eptaretus
264	237	7.6	1046	2	Q7PZJ7	ANOQA	Q7pzj7	anopheles g	337	226.5	7.2	298	2	Q4KF15	9PETR	Q4kpf15	ichthyomyzo
265	236.5	7.5	461	2	Q4SA12	TETNG	Q4sa12	tetraodon n	338	226.5	7.2	299	2	Q4GI19	EPTST	Q4gi19	eptaretus
266	236.5	7.5	715	2	Q4RY04	TETNG	Q4ry04	tetraodon n	339	226.5	7.2	323	2	Q32QI1	EPTST	Q32qi1	eptaretus
267	236	7.5	306	2	Q2YDZ7	EPTST	Q2ydz7	eptaretus	340	226.5	7.2	557	1	LG11	HUMAN	Q95970	homo sapien
268	236	7.5	707	1	LRRN3	MOUSE	Q8cb66	mus musculus	341	226.5	7.2	557	1	LRLFN5	PANTR	Q96n16	homo sapien
269	236	7.5	718	2	O6P6Z7	XENLA	Q6p6z7	xenopus lae	342	226.5	7.2	719	1	LRFN5	HUMAN	Q4kp16	ichthyomyzo
270	235.5	7.5	283	2	Q2YE20	EPTST	Q2ye20	eptaretus	343	226	7.2	321	2	Q4KF16	9PETR	Q4kp16	ichthyomyzo
271	235.5	7.5	296	2	Q4GIH6	EPTST	Q4gih6	eptaretus	344	226	7.2	322	2	Q32QN1	EPTST	Q32qn1	eptaretus
272	235.5	7.5	307	2	Q2YE19	EPTST	Q2ye19	eptaretus	345	226	7.2	364	2	Q4SQ63	TETNG	Q4sq63	tetraodon n
273	235.5	7.5	309	2	Q2YE00	EPTST	Q2ye00	eptaretus	346	225.5	7.2	210	2	Q4SCF1	TETNG	Q4scf1	tetraodon n
274	235.5	7.5	579	1	LRC15	MOUSE	Q80x72	mus musculus	347	225.5	7.2	257	2	Q2VGS2	PETWA	Q2vgs2	petromyzon
275	235	7.5	574	2	Q4RRR5	TETNG	Q4rrr5	tetraodon n	348	225.5	7.2	298	2	Q6E4J3	PETWA	Q6e4j3	petromyzon
276	234.5	7.5	346	2	Q32R33	EPTBU	Q32r33	eptaretus	349	225	7.1	733	2	Q2M032	DROPS	Q2m032	drosophila
277	234.5	7.5	488	2	Q4RK86	TETNG	Q4rk86	tetraodon n	350	224.5	7.2	323	2	Q32QSO	EPTST	Q32qso	eptaretus
278	234.5	7.5	703	2	Q16TC8	AEDAE	Q16tc8	aedes aegyp	351	224.5	7.2	347	2	Q32QO0	EPTST	Q32qo0	eptaretus
279	234.5	7.5	958	2	Q29LE3	DROPS	Q29le3	drosophila	352	224	7.1	218	2	Q2VGM8	PETWA	Q2vgm8	petromyzon
280	233.5	7.4	298	2	O6E4J4	PETWA	O6e4j4	petromyzon	353	224	7.1	322	2	Q32QR2	EPTST	Q32qr2	eptaretus
281	233.5	7.4	322	2	Q32Q21	EPTBU	Q32q21	eptaretus	354	224	7.1	1202	2	Q29I16	DROPS	Q29i16	drosophila
282	233.5	7.4	346	2	Q32Q19	EPTBU	Q32q19	eptaretus	355	223.5	7.1	209	2	Q2VXK5	PETWA	Q2vxs5	petromyzon
283	233.5	7.4	545	2	Q5R534	PONPY	Q5r534	pongo pygma	356	223.5	7.1	283	2	Q4GIH8	EPTST	Q4gih8	eptaretus
284	233.5	7.4	1587	2	Q17FD9	AEDAE	Q17fd9	aedes aegyp	357	223.5	7.1	323	2	Q2YE55	EPTST	Q2ye55	eptaretus
285	233	7.4	393	2	Q32R29	EPTBU	Q32r29	eptaretus	358	223.5	7.1	323	2	Q32QO0	EPTST	Q32qo0	eptaretus
286	233	7.4	1316	2	Q9V025	DROME	Q9v025	drosophila	359	223.5	7.1	647	2	Q4SIN0	TETNG	Q4sin0	tetraodon n
287	232.5	7.4	323	2	Q2YE85	EPTST	Q2ye85	eptaretus	360	223	7.1	289	2	Q6E4C8	PETWA	Q6e4c8	petromyzon
288	232	7.4	487	2	Q4SA13	TETNG	Q4sa13	tetraodon n	361	223	7.1	345	2	Q2YE83	EPTBU	Q2ye83	eptaretus
289	232	7.4	766	2	Q2WF71	MOUSE	Q2wf71	mus musculus	362	223	7.1	349	2	Q4SH52	TETNG	Q4sh52	tetraodon n
290	231.5	7.4	283	2	Q4GIH4	EPTST	Q4gih4	eptaretus	363	222.5	7.1	323	2	Q32QW5	EPTST	Q32qw5	eptaretus
291	231.5	7.4	323	2	Q2YE66	EPTST	Q2ye66	eptaretus	364	222.5	7.1	323	2	Q2YE67	EPTST	Q2ye67	eptaretus
292	231.5	7.4	323	2	Q32Q59	EPTST	Q32q59	eptaretus	365	222.5	7.1	323	2	Q32QV2	EPTST	Q32qv2	eptaretus
293	231.5	7.4	598	2	Q2PFK9	MACFA	Q2pfk9	macaca fasc	366	222.5	7.1	413	2	Q64Z15	MOUSE	Q64z15	mus musculus
294	231.5	7.4	840	1	SLIK6	MOUSE	Q8c110	mus musculus	367	222.5	7.1	557	1	LG11	RAT	Q84215	rattus norv
295	231	7.4	294	2	Q5VT99	HUMAN	Q5vt99	homo sapien	368	222.5	7.1	557	2	O5FWS7	RAT	Q5fws7	rattus norv
296	231	7.4	324	2	Q32QP7	EPTST	Q32qp7	eptaretus	369	222.5	7.1	557	2	O5FWS7	RAT	Q5fws7	rattus norv
297	231	7.4	347	2	Q32R08	EPTBU	Q32r08	eptaretus	370	222.5	7.1	792	2	Q90Z43	CHICK	Q90z43	gallus gall
298	231	7.4	547	1	CPN2	MOUSE	Q9dbb9	mus musculus	371	222	7.1	269	2	Q6E4I0	PETWA	Q6e4i0	petromyzon
299	231	7.4	581	2	Q49506	HUMAN	Q49506	homo sapien	372	222	7.1	348	2	Q95J08	MACFA	Q95jj8	macaca fasc
300	231	7.4	619	2	Q7QBW2	ANOQA	Q7qbw2	anopheles g	373	222	7.1	348	2	Q32QP2	EPTST	Q32qp2	eptaretus
301	231	7.4	766	2	Q460M4	MOUSE	Q460m4	mus musculus	374	222	7.1	348	2	Q32QN3	EPTST	Q32qn3	eptaretus
302	231	7.4	787	2	Q4SW26	TETNG	Q4sw26	tetraodon n	375	222	7.1	722	2	O5PPU2	XENLA	Q5ppu2	xenopus lae
303	230.5	7.4	257	2	Q2VGP9	PETWA	Q2vgs9	petromyzon	376	221.5	7.1	249	2	Q2VGK2	PETWA	Q2vgk2	petromyzon
304	230.5	7.4	323	2	Q32Q33	EPTST	Q32q33	eptaretus	377	221.5	7.1	323	2	Q32QV6	EPTST	Q32qv6	eptaretus
305	230.5	7.4	687	2	Q4SCX3	TETNG	Q4scx3	tetraodon n	378	221.5	7.1	323	2	Q32QW6	EPTST	Q32qw6	eptaretus
306	230	7.3	332	2	Q8QFN7	ELAQU	Q8qfn7	elaphe quad	379	221.5	7.1	475	2	Q4TI09	TETNG	Q4ti09	tetraodon n
307	230	7.3	332	2	Q8QFN6	ELAQU	Q8qfn6	elaphe quad	380	221.5	7.1	557	1	LG11	MOUSE	Q9fjia1	mus musculus
308	230	7.3	872	2	Q4SZ04	TETNG	Q4sz04	tetraodon n	381	221.5	7.1	719	1	LRFN5	MOUSE	Q8bxa0	mus musculus
309	230	7.3	1229	2	Q4T750	TETNG	Q4t750	tetraodon n	382	221.5	7.1	721	2	O5DTH4	MOUSE	O5dth4	mus musculus
310	229.5	7.3	233	2	Q2VGB3	PETWA	Q2vgs3	petromyzon	383	221	7.0	286	2	Q2YE07	EPTST	Q2ye07	eptaretus
311	229.5	7.3	323	2	Q2YEG5	EPTST	Q2yeg5	eptaretus	384	221	7.0	322	2	Q32Q55	EPTST	Q32q55	eptaretus
312	229.5	7.3	323	2	Q2YE70	EPTST	Q2ye70	eptaretus	385	221	7.0	345	2	Q32Q29	EPTBU	Q32q29	eptaretus
313	229.5	7.3	323	2	Q32QW0	EPTST	Q32qw0	eptaretus	386	221	7.0	348	2	Q32QV7	EPTST	Q32qv7	eptaretus
314	229.5	7.3	370	2	Q32R18	EPTBU	Q32r18	eptaretus	387	221	7.0	1091	1	LRI61	HUMAN	Q96jia1	homo sapien
315	229.5	7.3	828	2	Q8C8T7	MOUSE	Q8c8t7	mus musculus	388	221	7.0	1528	2	Q2UZU6	AEDAE	Q2uzu6	aedes aegyp
316	229	7.3	240	2	Q2VGN7	PETWA	Q2vgn7	petromyzon	389	220.5	7.0	210	2	Q6E4M1	PETWA	Q6e4m1	petromyzon
317	229	7.3	324	2	Q32Q75	EPTST	Q32qt5	eptaretus	390	220.5	7.0	306	2	Q4KP04	LAMAP	Q4kp04	lampetra ap
318	229	7.3	347	2	Q32R44	EPTBU	Q32r44	eptaretus	391	220.5	7.0	322	2	O6E4K1	PETWA	O6e4k1	petromyzon
319	229	7.3	348	2	Q32QW2	EPTST	Q32qw2	eptaretus	392	220.5	7.0	323	2	Q32QN5	EPTST	Q32qn5	eptaretus
320	229	7.3	581	1	LRC15	HUMAN	Q8tf66	homo sapien	393	220.5	7.0	342	2	Q4RW94	TETNG	Q4rw94	tetraodon n
321	228.5	7.3	294	2	O6E4I6	PETWA	O6e4i6	petromyzon	394	220.5	7.0	515	1	LRTW2	MOUSE	Q8bga3	mus musculus
322	228.5	7.3	341	1	LRC55	HUMAN	Q6zsa7	homo sapien	395	220.5	7.0	515	2	Q8C8L1	MOUSE	Q8c8l1	mus musculus
323	228.5	7.3	342	2	Q4RRU5	TETNG	Q4rru5	tetraodon n	396	220.5	7.0	733	2	Q24250	DROME	Q24250	drosophila

397	220.5	7.0	841	1	SLIK6_HUMAN	Q9h5Y7	homo sapien	470	213.5	6.8	1204	2	Q17K70_AEDAE	Q17K70	aedes aegypt
398	220	7.0	345	2	Q32R13_EPTBU	Q32R13	eptaretus	471	213	6.8	218	2	Q2VGT0_PETMA	Q2VGT0	petromyzon
399	220	7.0	347	2	Q32R23_EPTBU	Q32R23	eptaretus	472	213	6.8	322	2	Q32QX1_EPTST	Q32QX1	eptaretus
400	220	7.0	582	1	LRTM3_MOUSE	Q8bz81	mus musculus	473	213	6.8	323	2	Q32Q25_EPTBU	Q32Q25	eptaretus
401	220	7.0	582	2	Q8BZA0_MOUSE	Q8bz80	mus musculus	474	213	6.8	347	2	Q32R04_EPTBU	Q32R04	eptaretus
402	220	7.0	603	2	Q4SUZ7_TETNG	Q8sJ37	tetraodon n	475	213	6.8	716	1	LRRN1_MOUSE	Q61809	mus musculus
403	219.5	7.0	323	2	Q32QR3_EPTST	Q32qr3	eptaretus	476	213	6.8	811	2	Q17UT2_AEDAE	Q17J12	aedes aegypt
404	219.5	7.0	323	2	Q32Q74_EPTST	Q32qt4	eptaretus	477	212.5	6.8	323	2	Q32QS3_EPTST	Q32q3	eptaretus
405	219.5	7.0	323	2	Q32QW4_EPTST	Q32qw4	eptaretus	478	212.5	6.8	604	2	Q4SHE8_TETNG	Q4sH8	tetraodon n
406	219.5	7.0	323	2	Q32QV3_EPTST	Q32qv3	eptaretus	479	212	6.8	216	2	Q2VGU4_PETMA	Q2Vgu4	petromyzon
407	219.5	7.0	583	2	Q4SNQ0_TETNG	Q4snq0	tetraodon n	480	212	6.8	218	2	Q2VGI6_PETMA	Q2Vgi6	petromyzon
408	219	7.0	218	2	Q2VHI3_PETMA	Q2vh13	petromyzon	481	212	6.8	276	2	Q4GLJ9_EPTST	Q4glj9	eptaretus
409	219	7.0	264	2	Q2VH48_PETMA	Q2vh48	petromyzon	482	212	6.8	324	2	Q32QM9_EPTST	Q32qm9	eptaretus
410	219	7.0	324	2	Q2YF60_EPTST	Q2yef6	eptaretus	483	212	6.8	445	1	R4RL1_RAT	Q80W40	rattus norv
411	219	7.0	334	2	Q6P7C4_RAT	Q6p7c4	rattus norv	484	212	6.8	918	2	Q7Q3F0_ANOGA	Q7q3f0	anopheles g
412	218.5	7.0	322	2	Q32R19_EPTBU	Q32r19	eptaretus	485	211.5	6.7	192	2	Q6E419_PETMA	Q6e419	petromyzon
413	218.5	7.0	323	2	Q2YET6_EPTST	Q2ye76	eptaretus	486	211.5	6.7	270	2	Q6E417_PETMA	Q6e417	petromyzon
414	218.5	7.0	359	2	Q6GTU0_HUMAN	Q6gtu0	homo sapien	487	211.5	6.7	322	2	Q32R35_EPTBU	Q32r35	eptaretus
415	218.5	7.0	618	1	LRC21_MOUSE	Q8k099	mus musculus	488	211.5	6.7	323	2	Q2YE72_EPTST	Q2ye72	eptaretus
416	218	7.0	216	2	Q2VGH7_PETMA	Q2vgh7	petromyzon	489	211.5	6.7	323	2	Q32Q9_EPTST	Q32q9	eptaretus
417	218	7.0	264	2	Q2VGT2_PETMA	Q2vgt2	petromyzon	490	211.5	6.7	323	2	Q32Q97_EPTST	Q32q97	eptaretus
418	218	7.0	323	2	Q32R09_EPTBU	Q32r09	eptaretus	491	211.5	6.7	518	2	Q5R712_PONPY	Q5r712	pongo pygma
419	218	7.0	347	2	Q32R14_EPTBU	Q32r14	eptaretus	492	211.5	6.7	876	2	Q16190_AEDAE	Q16190	aedes aegypt
420	217.5	6.9	288	2	Q8BR15_MOUSE	Q8br15	mus musculus	493	211	6.7	187	2	Q6E412_PETMA	Q6e412	petromyzon
421	217.5	6.9	615	2	Q4SL87_TETNG	Q4sl87	tetraodon n	494	211	6.7	218	2	Q2VGR7_PETMA	Q2vgr7	petromyzon
422	217.5	6.9	695	2	Q4TIY8_TETNG	Q4tiy8	tetraodon n	495	211	6.7	581	1	LRTM3_HUMAN	Q86VH5	homo sapien
423	217.5	6.9	1335	2	Q610C7_CAEBR	Q610c7	caenorhabdi	496	211	6.7	581	1	LRTM3_MACFA	Q9bgp6	macaca fasc
424	217	6.9	322	2	Q2YB64_EPTST	Q2yeb4	eptaretus	497	211	6.7	581	2	Q2NKK7_HUMAN	Q2nkk7	homo sapien
425	217	6.9	348	2	Q32QM4_EPTST	Q32qm4	eptaretus	498	210.5	6.7	209	2	Q2VGR9_PETMA	Q2vgr9	petromyzon
426	217	6.9	637	2	Q6DCV7_XENLA	Q6dcv7	xenopus lae	499	210.5	6.7	257	2	Q4GLM3_EPTBU	Q4glm3	eptaretus
427	216.5	6.9	209	2	Q2VGT8_PETMA	Q2vgt8	petromyzon	500	210.5	6.7	321	2	Q6E415_PETMA	Q6e415	petromyzon
428	216	6.9	263	2	Q6E4C7_PETMA	Q6e4c7	petromyzon	501	210.5	6.7	322	2	Q32R37_EPTBU	Q32r37	eptaretus
429	216	6.9	282	2	Q4GL16_EPTST	Q4gl16	eptaretus	502	210.5	6.7	322	2	Q32R10_EPTBU	Q32r10	eptaretus
430	216	6.9	324	2	Q32QM1_EPTST	Q32qm1	eptaretus	503	210.5	6.7	4303	1	PKD1_HUMAN	P98161	homo sapien
431	216	6.9	324	2	Q32QW4_EPTST	Q32qw4	eptaretus	504	210	6.7	264	2	Q2VGI2_PETMA	Q2vgi2	petromyzon
432	216	6.9	514	2	Q4VBX1_MOUSE	Q4vbx1	mus musculus	505	210	6.7	324	2	Q2YE50_EPTST	Q2ye50	eptaretus
433	215.5	6.9	322	2	Q32R32_EPTBU	Q32r32	eptaretus	506	210	6.7	324	2	Q32QU4_EPTST	Q32qu4	eptaretus
434	215.5	6.9	323	2	Q32Q76_EPTST	Q32q76	eptaretus	507	210	6.7	324	2	Q32Q70_EPTST	Q32q70	eptaretus
435	215.5	6.9	323	2	Q2YB61_EPTST	Q2yeb1	eptaretus	508	210	6.7	324	2	Q32Q82_EPTST	Q32q82	eptaretus
436	215.5	6.9	329	2	Q56NG5_CIOIN	Q56ng5	ciona intes	509	210	6.7	358	1	CHAD_RAT	Q70210	rattus norv
437	215.5	6.9	331	1	FLIB_AGRBL	Q932J3	agkistrodon	510	210	6.7	1028	2	Q865R7_PIG	Q865r7	sus scrofa
438	215.5	6.9	612	2	Q4SYK9_TETNG	Q4syk9	tetraodon n	511	209.5	6.7	214	2	Q6E4H0_PETMA	Q6e4h0	petromyzon
439	215.5	6.9	737	2	Q9VU51_DROME	Q9vu51	drosophila	512	209.5	6.7	322	2	Q32R06_EPTBU	Q32r06	eptaretus
440	215	6.9	322	2	Q32QX8_EPTST	Q32qx8	eptaretus	513	209.5	6.7	322	2	Q32R12_EPTBU	Q32r12	eptaretus
441	215	6.9	323	2	Q2YB53_EPTST	Q2yeb3	eptaretus	514	209.5	6.7	323	2	Q32Q08_EPTST	Q32q08	eptaretus
442	215	6.9	323	2	Q32QV8_EPTBU	Q32qv8	eptaretus	515	209.5	6.7	323	2	Q32Q81_EPTST	Q32q81	eptaretus
443	215	6.9	323	2	Q32R00_EPTBU	Q32r00	eptaretus	516	209.5	6.7	323	2	Q32QU6_EPTST	Q32qu6	eptaretus
444	215	6.9	323	2	Q32Q00_EPTST	Q32q00	eptaretus	517	209.5	6.7	382	2	Q1EGK9_PANTR	Q1egk9	pan troglod
445	215	6.9	324	2	Q32Q04_EPTST	Q32q04	eptaretus	518	209.5	6.7	533	2	Q5E9T6_BOVIN	Q5e9t6	bos taurus
446	215	6.9	743	2	Q6P1M7_HUMAN	Q6plm7	homo sapien	519	209	6.7	211	2	Q6E413_PETMA	Q6e413	petromyzon
447	214.5	6.8	215	2	Q2VH33_PETMA	Q2vh33	petromyzon	520	209	6.7	216	2	Q2VQG6_PETMA	Q2vqg6	petromyzon
448	214.5	6.8	323	2	Q32QR4_EPTST	Q32qr4	eptaretus	521	209	6.7	257	2	Q6E4J6_PETMA	Q6e4j6	petromyzon
449	214.5	6.8	323	2	Q32QR6_EPTST	Q32qr6	eptaretus	522	209	6.7	322	2	Q32QM8_EPTST	Q32qm8	eptaretus
450	214.5	6.8	323	2	Q32QP5_EPTST	Q32qp5	eptaretus	523	209	6.7	323	2	Q32R01_EPTBU	Q32r01	eptaretus
451	214.5	6.8	329	2	Q56NG6_CIOIN	Q56ng6	ciona intes	524	209	6.7	358	1	CHAD_MOUSE	Q55226	mus musculus
452	214.5	6.8	347	2	Q32QP1_EPTST	Q32qp1	eptaretus	525	209	6.7	358	2	Q5SUU4_MOUSE	Q5suu4	mus musculus
453	214.5	6.8	441	1	R4RL1_HUMAN	Q86un2	homo sapien	526	209	6.7	391	2	Q4S8B7_TETNG	Q4s8b7	tetraodon n
454	214.5	6.8	716	1	LRRN1_HUMAN	Q8uxk5	homo sapien	527	209	6.7	1091	1	LRIG1_MOUSE	P70193	mus musculus
455	214.5	6.8	731	2	Q4TI49_TETNG	Q4ti49	tetraodon n	528	209	6.7	1262	2	Q29L45_DROPS	Q29l45	drosophila
456	214.5	6.8	1535	2	Q23991_DROME	Q23991	drosophila	529	208.5	6.7	350	2	QSRH06_BRARE	Qsrh06	brachydanio
457	214	6.8	295	2	Q6E4C9_PETMA	Q6e4c9	petromyzon	530	208.5	6.7	382	1	PRELP_HUMAN	P51888	homo sapien
458	214	6.8	323	2	Q32R42_EPTBU	Q32r42	eptaretus	531	208.5	6.7	382	2	Q6FHG6_HUMAN	Q6fhg6	homo sapien
459	214	6.8	324	2	Q2YB68_EPTST	Q2yeb68	eptaretus	532	208.5	6.7	382	2	Q6FG38_HUMAN	Q6fg38	homo sapien
460	214	6.8	516	1	LRTM2_HUMAN	Q43300	homo sapien	533	208.5	6.7	445	1	R4RL1_MOUSE	Q8k085	mus musculus
461	214	6.8	716	1	LRRN1_RAT	Q32q07	rattus norv	534	208.5	6.7	479	2	Q6X3Y5_BRARE	Q6x3y5	brachydanio
462	214	6.8	717	2	Q4SR34_TETNG	Q4sr34	tetraodon n	535	208.5	6.7	518	1	LRTM4_HUMAN	Q86vH4	homo sapien
463	214	6.8	2828	2	Q9NR39_HUMAN	Q9nr39	homo sapien	536	208.5	6.7	518	2	Q4FZ98_HUMAN	Q4fz98	homo sapien
464	213.5	6.8	282	2	Q6E4J5_PETMA	Q6e4j5	petromyzon	537	208.5	6.7	519	2	Q4KMX1_HUMAN	Q4kxm1	homo sapien
465	213.5	6.8	259	2	Q2YB23_EPTST	Q2yeb23	eptaretus	538	208.5	6.7	537	1	LG14_HUMAN	Q8n135	homo sapien
466	213.5	6.8	273	2	Q4GL12_EPTBU	Q4gl12	eptaretus	539	208.5	6.7	530	2	Q6UXJ7_HUMAN	Q6uxj7	homo sapien
467	213.5	6.8	323	2	Q32QM9_EPTST	Q32qm9	eptaretus	540	208	6.6	218	2	Q2VGF5_PETMA	Q2vgf5	petromyzon
468	213.5	6.8	359	1	CHAD_HUMAN	Q15335	homo sapien	541	208	6.6	322	2	Q2YE51_EPTST	Q2ye51	eptaretus
469	213.5	6.8	361	1	CHAD_BOVIN	Q27972	bos taurus	542	208	6.6	649	2	Q9VK22_DROME	Q9vk22	drosophila

543	207.5	6.6	180	2	Q6E4F0_PETWA	Q6E4F0_PETROMYZON	616	203	6.5	602	1	LRC40_MACPA	Q4r3p6 macaca fasc
544	207.5	6.6	323	2	Q32Q12_EPTST	Q32q12 eptatretus	617	203	6.5	703	2	Q4SLZ4_TETNG	Q4slz4 tetraodon n
545	207.5	6.6	330	2	Q4S074_TETNG	Q4s074 tetraodon n	618	203	6.5	1514	2	Q9NBK9_DROME	Q9nbk9 drosophila
546	207.5	6.6	518	2	Q6ZT31_HUMAN	Q6zt31 homo sapien	619	203	6.5	1514	2	Q6NN49_DROME	Q6nn49 drosophila
547	207.5	6.6	610	2	Q17G04_AEDAE	Q17gd4 aedes aegyp	620	203	6.5	1514	2	Q9VUN0_DROME	Q9vun0 drosophila
548	207.5	6.6	1329	1	GP124_MOUSE	Q91zv8 mus musculu	621	202.5	6.5	197	2	Q2VGR8_PETWA	Q2vgr8 petromyzon
549	207	6.6	313	1	LRC52_HUMAN	Q8n7c0 homo sapien	622	202.5	6.5	209	2	Q2VGV9_PETWA	Q2vgr9 petromyzon
550	207	6.6	323	2	Q2YE80_EPTBU	Q2ye80 eptatretus	623	202.5	6.5	259	2	Q4GIH5_EPTST	Q4gh5 eptatretus
551	207	6.6	323	2	Q32R43_EPTBU	Q32r43 eptatretus	624	202.5	6.5	259	2	Q4GIK1_EPTST	Q4gik1 eptatretus
552	207	6.6	536	2	Q6P0D2_BRARE	Q6p0d2 brachydanio	625	202.5	6.5	274	2	Q6E4J2_PETWA	Q6e4j2 petromyzon
553	207	6.6	537	2	Q2HPG2_BRARE	Q2hpg2 brachydanio	626	202.5	6.5	329	2	Q32Q28_EPTBU	Q32q28 eptatretus
554	207	6.6	613	2	Q50L44_CHICK	Q50l44 gallus gall	627	202.5	6.5	822	2	Q4RIG0_TETNG	Q4rig0 tetraodon n
555	207	6.6	740	1	CT075_HUMAN	Q8wut4 homo sapien	628	202	6.4	271	2	Q4KP11_LAMAP	Q4kpl1 lampetra ap
556	207	6.6	4293	2	Q08852_MOUSE	Q08852 mus musculu	629	202	6.4	300	2	Q2YE57_EPTST	Q2ye57 eptatretus
557	206.5	6.6	192	2	Q2VGS9_PETWA	Q2vgs9 petromyzon	630	202	6.4	321	2	Q32R36_EPTBU	Q32r36 eptatretus
558	206.5	6.6	270	2	Q6E4K6_PETWA	Q6e4k6 petromyzon	631	202	6.4	321	2	Q32R38_EPTBU	Q32r38 eptatretus
559	206.5	6.6	274	2	Q6E4C1_PETWA	Q6e4c1 petromyzon	632	202	6.4	324	2	Q32Q58_EPTST	Q32q58 eptatretus
560	206.5	6.6	274	2	Q6E4B9_PETWA	Q6e4b9 petromyzon	633	202	6.4	1117	2	Q5VOM7_ORYSA	Q5vom7 oryza sativ
561	206.5	6.6	294	2	Q6E4L2_PETWA	Q6e4l2 petromyzon	634	202	6.4	1501	2	Q2MIB4_DROPS	Q2mlb4 drosophila
562	206.5	6.6	323	2	Q32Q08_EPTST	Q32q08 eptatretus	635	201.5	6.4	187	2	Q6E4D7_PETWA	Q6e4d7 petromyzon
563	206.5	6.6	327	2	Q5U4S7_XENLA	Q5u4s7 xenopus lae	636	201.5	6.4	275	2	Q4GIJ5_EPTST	Q4gij5 eptatretus
564	206.5	6.6	614	2	Q9D1T0_MOUSE	Q9d1t0 mus musculu	637	201.5	6.4	457	2	Q960D1_DROME	Q960d1 drosophila
565	206	6.6	218	2	Q2VGU6_PETWA	Q2vgu6 petromyzon	638	201.5	6.4	524	2	Q4RP59_TETNG	Q4rf59 tetraodon n
566	206	6.6	324	2	Q32QX7_EPTST	Q32qx7 eptatretus	639	201.5	6.4	551	2	Q4RP95_TETNG	Q4rf95 tetraodon n
567	206	6.6	353	1	TSK_HUMAN	Q8wua8 homo sapien	640	201.5	6.4	606	2	Q9BZ20_HUMAN	Q9bz20 homo sapien
568	206	6.6	381	1	PREUJ_BOVIN	Q9gkn8 bos taurus	641	201.5	6.4	892	2	P91644_DROME	P91644 drosophila
569	206	6.6	428	1	Q14498_HUMAN	Q14498 homo sapien	642	201.5	6.4	1527	2	Q9VZZ4_DROME	Q9vzz4 drosophila
570	206	6.6	539	2	Q5TPW2_ANOGA	Q5tpw2 anopheles g	643	201	6.4	213	2	Q6E4H6_PETWA	Q6e4h6 petromyzon
571	206	6.6	606	2	Q3URE9_MOUSE	Q3ure9 mus musculu	644	201	6.4	218	2	Q6E4K9_PETWA	Q6e4k9 petromyzon
572	206	6.6	606	2	Q8BLC0_MOUSE	Q8blc0 m adult mal	645	201	6.4	322	2	Q32Q11_EPTST	Q32q11 eptatretus
573	206	6.6	606	2	Q8BZD4_MOUSE	Q8bzd4 mus musculu	646	201	6.4	336	2	Q4S8M5_TETNG	Q4s8m5 tetraodon n
574	206	6.6	738	2	Q5UIA7_DROME	Q5uia7 drosophila	647	201	6.4	354	1	TSK_MOUSE	Q8cbr6 mus musculu
575	206	6.6	1054	1	LRIQ2_MOUSE	Q52kr2 mus musculu	648	201	6.4	602	1	LRC40_HUMAN	Q9h9a6 homo sapien
576	206	6.6	1127	2	Q4TAT5_TETNG	Q4tat9 tetraodon n	649	201	6.4	712	2	Q5BL20_BRARE	Q5bl20 brachydanio
577	205.5	6.6	212	2	Q6E4H2_PETWA	Q6e4h2 petromyzon	650	201	6.4	1391	2	Q29C89_DROPS	Q29c89 drosophila
578	205.5	6.6	479	2	Q6D7H6_BRARE	Q6d7h6 brachydanio	651	200.5	6.4	835	1	Q29MX7_DROPS	Q29mx7 drosophila
579	205.5	6.6	492	2	Q99KT6_MOUSE	Q99kt6 mus musculu	652	200.5	6.4	845	1	SLIK2_HUMAN	Q9h156 homo sapien
580	205.5	6.6	590	1	LRTM4_MOUSE	Q80xg9 mus musculu	653	200.5	6.4	845	2	Q2KHN3_HUMAN	Q2khn3 homo sapien
581	205	6.5	248	2	Q4GIK4_EPTST	Q4gik4 eptatretus	654	200.5	6.4	1336	2	Q2XXV6_DROYA	Q2xxv7 drosophila
582	205	6.5	256	2	Q4GI16_EPTBU	Q4gi16 eptatretus	655	200.5	6.4	1337	2	Q2XXV7_DROYA	Q2xxv7 drosophila
583	205	6.5	320	2	Q32OR9_EPTST	Q32or9 eptatretus	656	200	6.4	218	2	Q2VGV1_PETWA	Q2vgv1 petromyzon
584	205	6.5	322	2	Q2YB54_EPTST	Q2ye54 eptatretus	657	200	6.4	280	2	Q2YE26_EPTBU	Q2ye26 eptatretus
585	205	6.5	322	2	Q2YB83_EPTST	Q2ye83 eptatretus	658	200	6.4	460	2	Q4RK03_TETNG	Q4rk03 tetraodon n
586	205	6.5	322	2	Q32Q06_EPTST	Q32q06 eptatretus	659	200	6.4	547	2	Q1EGK1_FUGRU	Q1egk1 fugu rubrip
587	205	6.5	324	2	Q2YB84_EPTST	Q2ye84 eptatretus	660	200	6.4	616	2	Q58A95_CAEL	Q58a95 caenorhabdi
588	205	6.5	486	2	Q4RU74_TETNG	Q4ru74 tetraodon n	661	200	6.4	653	2	Q02329_CAEL	Q02329 caenorhabdi
589	205	6.5	614	2	Q5RDJ4_PONPY	Q5rdj4 pongo pygma	662	199.5	6.4	227	2	Q4SP28_TETNG	Q4sp28 tetraodon n
590	205	6.5	620	2	Q9N008_MACPA	Q9n008 macaca fasc	663	199.5	6.4	261	2	Q4GI14_EPTBU	Q4gi14 eptatretus
591	205	6.5	620	2	Q96FE5_HUMAN	Q96fes homo sapien	664	199.5	6.4	319	2	Q32QN9_EPTST	Q32qn9 eptatretus
592	204.5	6.5	322	2	Q32R03_EPTBU	Q32r03 eptatretus	665	199.5	6.4	622	2	Q66HV9_BRARE	Q66hv9 brachydanio
593	204.5	6.5	323	2	Q32Q02_EPTST	Q32q02 eptatretus	666	199	6.3	260	2	Q2YE05_EPTST	Q2ye05 eptatretus
594	204.5	6.5	463	2	Q8CIV9_MOUSE	Q8civ9 mus musculu	667	199	6.3	298	2	Q32QW3_EPTST	Q32qw3 eptatretus
595	204	6.5	196	2	Q2VGM9_PETWA	Q2vgm9 petromyzon	668	199	6.3	322	2	Q32QV5_EPTST	Q32qv5 eptatretus
596	204	6.5	276	2	Q2YB25_EPTST	Q2ye25 eptatretus	669	199	6.3	323	2	Q32QV8_EPTST	Q32qv8 eptatretus
597	204	6.5	323	2	Q32R20_EPTBU	Q32r20 eptatretus	670	199	6.3	323	2	Q32R07_EPTBU	Q32r07 eptatretus
598	204	6.5	323	2	Q2YB81_EPTBU	Q2ye81 eptatretus	671	199	6.3	323	2	Q32QY5_EPTBU	Q32qy5 eptatretus
599	204	6.5	353	1	TSK_RAT	Q6gmy6 rattus norv	672	199	6.3	323	2	Q32R24_EPTBU	Q32r24 eptatretus
600	204	6.5	1173	2	Q9V7J8_DROME	Q9v7j8 drosophila	673	199	6.3	324	2	Q32Q17_EPTST	Q32q17 eptatretus
601	204	6.5	1306	2	Q6P4S1_XENLA	Q6p4s1 xenopus lae	674	199	6.3	846	1	SLIK2_MOUSE	Q810c0 mus musculu
602	203.5	6.5	219	2	Q2VG22_PETWA	Q2vg22 petromyzon	675	199	6.3	862	2	Q4SST3_TETNG	Q4sst3 tetraodon n
603	203.5	6.5	299	2	Q32GX3_EPTST	Q32gx3 eptatretus	676	199	6.3	1328	2	Q21043_CAEL	Q21043 caenorhabdi
604	203.5	6.5	845	2	Q6AI13_HUMAN	Q6ai13 homo sapien	677	198.5	6.3	259	2	Q4GIJ4_EPTST	Q4gij4 eptatretus
605	203.5	6.5	894	2	Q9VKG1_DROME	Q9vkg1 drosophila	678	198.5	6.3	320	2	Q6YNA4_HUMAN	Q6yna4 homo sapien
606	203.5	6.5	1061	2	Q53ME4_ORYSA	Q53me4 oryza sativ	679	198.5	6.3	322	2	Q32R17_EPTBU	Q32r17 eptatretus
607	203.5	6.5	1065	1	LRIQ2_HUMAN	Q94898 homo sapien	680	198.5	6.3	548	2	Q1EG10_PANTR	Q1eg10 pan troglod
608	203	6.5	218	2	Q2VGC8_PETWA	Q2vgc8 petromyzon	681	198.5	6.3	617	1	LRC21_RAT	Q9jml2 rattus norv
609	203	6.5	269	2	Q6E4B6_PETWA	Q6e4b6 petromyzon	682	198.5	6.3	741	2	Q4SWG9_TETNG	Q4swg9 tetraodon n
610	203	6.5	286	2	Q2YE17_EPTST	Q2ye17 eptatretus	683	198.5	6.3	873	2	Q7XR24_ORYSA	Q7xr24 oryza sativ
611	203	6.5	321	2	Q32Q24_EPTBU	Q32q24 eptatretus	684	198.5	6.3	1331	1	GP124_HUMAN	Q96p1 homo sapien
612	203	6.5	323	2	Q32R15_EPTBU	Q32r15 eptatretus	685	198	6.3	192	2	Q2VH08_PETWA	Q2vh08 petromyzon
613	203	6.5	324	2	Q32QR5_EPTST	Q32qr5 eptatretus	686	198	6.3	298	2	Q32QN7_EPTST	Q32qn7 eptatretus
614	203	6.5	324	2	Q2YE71_EPTST	Q2ye71 eptatretus	687	198	6.3	322	2	Q32QP4_EPTST	Q32qp4 eptatretus
615	203	6.5	428	2	Q5NVQ6_PONPY	Q5nvq6 pongo pygma	688	198	6.3	323	2	Q32R16_EPTBU	Q32r16 eptatretus

689	198	6.3	323	2	Q32R22_EPTBU	Q32r22 eptatretus	762	193.5	6.2	545	1	LGI2_HUMAN	Q8n0v4 homo sapien
690	198	6.3	324	2	Q32Q8_EPTST	Q32q8 eptatretus	763	193.5	6.2	545	2	Q3MIN2_HUMAN	Q3min2 homo sapien
691	198	6.3	363	2	Q7SV85_BRARE	Q7sy85 brachydanio	764	193.5	6.2	545	2	Q1EGL1_PANTR	Q1egl1 pan troglod
692	198	6.3	602	1	LRC40_PONPY	Q5rf69 pongo pygma	765	193.5	6.2	574	2	Q60W68_CAEBR	Q60w68 caenorhabdi
693	197.5	6.3	193	2	Q2VGP6_PETWA	Q2vgp6 petromyzon	766	193.5	6.2	721	1	Y2082_MYCTU	Q10690 mycobacteri
694	197.5	6.3	280	2	Q6E4K3_PETWA	Q6e4k3 petromyzon	767	193.5	6.2	721	2	Q7T224_MYCBO	Q7t224 mycobacteri
695	197.5	6.3	300	2	Q6E4K8_PETWA	Q6e4k8 petromyzon	768	193.5	6.2	816	2	Q1KL20_FUGRU	Q1kl20 fugu rubrip
696	197.5	6.3	323	2	Q32QK3_EPTST	Q32qk3 eptatretus	769	193.5	6.2	863	2	Q46A62_METBF	Q46a62 methanosarc
697	197.5	6.3	441	2	Q4VB23_HUMAN	Q4ve23 homo sapien	770	193.5	6.2	881	2	Q2XY26_DROME	Q2xy26 drosophila
698	197.5	6.3	537	2	Q9VE49_DROME	Q9ve49 drosophila	771	193.5	6.2	881	2	Q2XY24_DROSI	Q2xy24 drosophila
699	197.5	6.3	548	1	LGI3_HUMAN	Q8n145 homo sapien	772	193.5	6.2	910	1	PIDD_HUMAN	Q3hb75 homo sapien
700	197.5	6.3	548	2	Q4R4H3_MACFA	Q4r4h3 macaca fasc	773	193.5	6.2	967	2	Q3UWD5_MOUSE	Q3uwd5 mus musculu
701	197.5	6.3	818	2	Q4SIX2_TETNG	Q4s1x2 tetraodon n	774	193.5	6.2	977	1	SLIK3_HUMAN	Q34933 homo sapien
702	197.5	6.3	835	2	Q4SFB0_TETNG	Q4sfb0 tetraodon n	775	193.5	6.2	977	2	Q1RMY6_HUMAN	Q1rmv6 homo sapien
703	197.5	6.3	1321	1	GP125_HUMAN	Q81wk6 homo sapien	776	193.5	6.2	1333	2	Q2XXV8_DROSI	Q2xxv8 drosophila
704	197	6.3	248	2	Q2YB16_EPTST	Q2yeb16 eptatretus	777	193.5	6.2	1333	2	Q2XXV9_DROSI	Q2xxv9 drosophila
705	197	6.3	320	2	Q32Q9_EPTST	Q32q9 eptatretus	778	193	6.2	252	2	Q4G112_EPTST	Q4g112 eptatretus
706	197	6.3	322	2	Q32Q6_EPTST	Q32q6 eptatretus	779	193	6.2	319	2	Q32R40_EPTBU	Q32r40 eptatretus
707	197	6.3	345	2	Q9HBL6_HUMAN	Q9hb16 homo sapien	780	193	6.2	321	2	Q32R11_EPTBU	Q32r11 eptatretus
708	197	6.3	694	2	Q6YXX5_ORYSA	Q6yxx5 oryza sativ	781	193	6.2	334	2	Q32Q2_EPTST	Q32q2 eptatretus
709	197	6.3	1093	2	Q5XWD3_HUMAN	Q5xw3 homo sapien	782	193	6.2	497	2	Q4SZU8_TETNG	Q4szu8 tetraodon n
710	196.5	6.3	209	2	Q2VGH6_PETWA	Q2vgh6 petromyzon	783	193	6.2	538	2	Q2LZK6_DROPS	Q2lzk6 drosophila
711	196.5	6.3	259	2	Q4GIJ3_EPTST	Q4gi13 eptatretus	784	193	6.2	545	2	Q2HFP8_BRARE	Q2hpf8 brachydanio
712	196.5	6.3	259	2	Q2YB12_EPTST	Q2yeb12 eptatretus	785	193	6.2	550	2	Q9VUN8_DROME	Q9vjn8 drosophila
713	196.5	6.3	261	2	Q4GIJ1_EPTST	Q4gi11 eptatretus	786	193	6.2	743	2	Q17AC3_ABDAB	Q17ac3 aedes aegyp
714	196.5	6.3	322	2	Q32QV4_EPTBU	Q32qv4 eptatretus	787	192.5	6.1	185	2	Q2VGZ4_PETWA	Q2vgz4 petromyzon
715	196.5	6.3	551	2	Q2LZ92_DROPS	Q2lzk6 drosophila	788	192.5	6.1	187	2	Q6E4D5_PETWA	Q6e4d5 petromyzon
716	196.5	6.3	1332	2	Q2XXV5_DROER	Q2xxv5 drosophila	789	192.5	6.1	195	2	Q2VH18_PETWA	Q2vh18 petromyzon
717	196.5	6.3	1333	2	Q2XXW0_DROME	Q2xxw0 drosophila	790	192.5	6.1	214	2	Q6E4G0_PETWA	Q6e4g0 petromyzon
718	196	6.3	263	2	Q6E4D0_PETWA	Q6e4d0 petromyzon	791	192.5	6.1	259	2	Q4G1H7_EPTST	Q4g1h7 eptatretus
719	196	6.3	300	2	Q32QX6_EPTST	Q32qx6 eptatretus	792	192.5	6.1	270	2	Q6E4K0_PETWA	Q6e4k0 petromyzon
720	196	6.3	3638	2	Q15142_HUMAN	Q15142 homo sapien	793	192.5	6.1	299	2	Q32QV1_EPTST	Q32qv1 eptatretus
721	195.5	6.2	274	2	Q1EGJ6_CHICK	Q1eg16 gallus gall	794	192.5	6.1	322	2	Q32QY3_EPTBU	Q32qy3 eptatretus
722	195.5	6.2	298	2	Q32Q26_EPTBU	Q32q26 eptatretus	795	192.5	6.1	428	2	Q6GU58_MOUSE	Q6gu58 mus musculu
723	195.5	6.2	323	2	Q2YB59_EPTST	Q2yeb59 eptatretus	796	192.5	6.1	542	2	Q50DZ7_MOUSE	Q50dz7 mus musculu
724	195.5	6.2	370	2	Q58D17_BOVIN	Q58d17 bos taurus	797	192.5	6.1	575	2	Q23580_CAEBL	Q23580 caenorhabdi
725	195.5	6.2	378	1	PRELP_MOUSE	Q9jfk53 mus musculu	798	192.5	6.1	887	2	Q2XY21_DROER	Q2xy21 drosophila
726	195.5	6.2	378	2	Q54380_MOUSE	Q54380 mus musculu	799	192.5	6.1	1093	2	Q6HA06_CRAGI	Q6ha06 crassostrea
727	195.5	6.2	543	2	Q29KW0_DROPS	Q29kw0 drosophila	800	192	6.1	265	2	Q6E4K2_PETWA	Q6e4k2 petromyzon
728	195.5	6.2	917	2	Q86PM1_DROME	Q86pm1 drosophila	801	192	6.1	273	2	Q6E4C5_PETWA	Q6e4c5 petromyzon
729	195.5	6.2	931	2	Q9VW16_DROME	Q9vw16 drosophila	802	192	6.1	300	2	Q2YB86_EPTST	Q2yeb86 eptatretus
730	195	6.2	322	2	Q32Q99_EPTST	Q32qp9 eptatretus	803	192	6.1	548	1	LGI3_MOUSE	Q8k406 mus musculu
731	195	6.2	440	2	Q4R5H2_MACFA	Q4r5h2 macaca fasc	804	192	6.1	548	2	Q3V1R3_MOUSE	Q3v1r3 mus musculu
732	195	6.2	526	2	Q1EGJ8_CHICK	Q1eg18 gallus gall	805	192	6.1	627	2	Q6UN14_LEICH	Q6un14 leishmania
733	195	6.2	614	2	Q6NUK3_HUMAN	Q6nuk3 homo sapien	806	191.5	6.1	185	2	Q2VGS8_PETWA	Q2vgs8 petromyzon
734	195	6.2	620	2	Q6UXN3_HUMAN	Q6uxn3 homo sapien	807	191.5	6.1	187	2	Q6E417_PETWA	Q6e417 petromyzon
735	195	6.2	837	1	SLIK4_HUMAN	Q81w52 homo sapien	808	191.5	6.1	193	2	Q2VGY8_PETWA	Q2vgy8 petromyzon
736	195	6.2	837	2	Q5JXG3_HUMAN	Q5jxg3 homo sapien	809	191.5	6.1	204	2	Q6E4J8_PETWA	Q6e4j8 petromyzon
737	195	6.2	1536	2	Q29DD0_DROPS	Q29dd0 drosophila	810	191.5	6.1	915	1	PIDD_MOUSE	Q9erv7 mus musculu
738	194.5	6.2	322	2	Q2YB92_EPTBU	Q2yeb92 eptatretus	811	191.5	6.1	980	1	SLIK3_MOUSE	Q810b9 mus musculu
739	194.5	6.2	323	2	Q32QV9_EPTST	Q32qv9 eptatretus	812	191.5	6.1	980	2	Q6NZM5_MOUSE	Q6nzm5 mus musculu
740	194.5	6.2	369	1	TSK_CHICK	Q85z91 gallus gall	813	191	6.1	192	2	Q2VGN8_PETWA	Q2vgn8 petromyzon
741	194.5	6.2	680	2	Q3MH9_BOVIN	Q3mhn9 bos taurus	814	191	6.1	194	2	Q2VGE8_PETWA	Q2vge8 petromyzon
742	194.5	6.2	693	2	Q7Z3D0_HUMAN	Q7z3d0 homo sapien	815	191	6.1	271	2	Q4KFP0_LAMAP	Q4kfp0 lampetra ap
743	194.5	6.2	699	1	ECM2_HUMAN	Q94769 homo sapien	816	191	6.1	440	2	Q5RC08_PONPY	Q5rc08 pongo pygma
744	194.5	6.2	699	2	Q5T9F2_HUMAN	Q5t9f2 homo sapien	817	191	6.1	456	2	Q28XA4_DROPS	Q28xa4 drosophila
745	194.5	6.2	737	2	Q965M3_CAEBL	Q965m3 caenorhabdi	818	191	6.1	536	2	Q173K1_AEDAE	Q173k1 aedes aegyp
746	194.5	6.2	881	2	Q965H2_CAEBL	Q965h2 caenorhabdi	819	191	6.1	610	2	Q4TIM0_TETNG	Q4tlm0 tetraodon n
747	194.5	6.2	1630	1	LAP4_HUMAN	Q14160 homo sapien	820	191	6.1	757	2	Q28XQ2_DROPS	Q28xq2 drosophila
748	194	6.2	192	2	Q2VGV7_PETWA	Q2vgv7 petromyzon	821	191	6.1	868	2	Q2XQ10_CHICK	Q2xq10 gallus gall
749	194	6.2	258	2	Q4GIJ7_EPTST	Q4gi17 eptatretus	822	190.5	6.1	251	2	Q4G117_EPTST	Q4g117 eptatretus
750	194	6.2	258	2	Q4G110_EPTST	Q4g110 eptatretus	823	190.5	6.1	536	2	Q2HFG1_BRARE	Q2hpg1 brachydanio
751	194	6.2	263	2	Q6E4C0_PETWA	Q6e4c0 petromyzon	824	190.5	6.1	894	2	Q5H721_FUGRU	Q5h721 fugu rubrip
752	194	6.2	320	2	Q32Q73_EPTST	Q32q73 eptatretus	825	190.5	6.1	1218	2	Q6NR19_DROME	Q6nr19 drosophila
753	194	6.2	611	2	Q4RHK3_TETNG	Q4rhk3 tetraodon n	826	190.5	6.1	1343	2	Q9VPF0_DROME	Q9vpf0 drosophila
754	194	6.2	692	2	Q4RV46_TETNG	Q4rv46 tetraodon n	827	190.5	6.1	1535	2	Q9VFG3_PETWA	Q9vfg3 petromyzon
755	194	6.2	836	2	Q9V9V6_DROME	Q9v9v6 drosophila	828	190	6.1	191	2	Q6E4H3_PETWA	Q6e4h3 petromyzon
756	193.5	6.2	186	2	Q6E4H8_PETWA	Q6e4h8 petromyzon	829	190	6.1	536	2	Q16P99_AEDAE	Q16p99 aedes aegyp
757	193.5	6.2	270	2	Q4KPO3_LAMAP	Q4kpo3 lampetra ap	830	190	6.1	639	2	Q4R568_TETNG	Q4r568 tetraodon n
758	193.5	6.2	273	2	Q4GLM1_EPTBU	Q4glm1 eptatretus	831	190	6.1	654	2	Q628N6_CAEBR	Q628n6 caenorhabdi
759	193.5	6.2	377	1	PRELP_RAT	Q9eqp5 rattus norv	832	190	6.1	733	1	CT075_MOUSE	P59383 mus musculu
760	193.5	6.2	378	2	Q8CAZ9_MOUSE	Q8caz9 mus musculu	833	190	6.1	1119	1	LRIG3_HUMAN	Q6uxm1 homo sapien
761	193.5	6.2	433	2	Q6IDG7_DROME	Q6idg7 drosophila	834	190	6.1	1346	2	Q9V477_DROME	Q9v477 drosophila

835	190	6.1	2800	2	Q6XHB1_DICDI	Q6xbh1 dictyosteli	908	185.5	5.9	185	2	Q2VGV1_PETMA	Q2vgv1 petromyzon
836	190	6.1	2800	2	Q1ZXD6_DICDI	Q1zxd6 dictyosteli	909	185.5	5.9	191	2	Q2VGC6_PETMA	Q2vgc6 petromyzon
837	189.5	6.0	2822	2	Q4GJL7_EPTST	Q4gj7 eptatretus	910	185.5	5.9	191	2	Q2VGR0_PETMA	Q2vgr0 petromyzon
838	189.5	6.0	370	2	Q4RSX9_TETNG	Q4rsx9 tetraodon n	911	185.5	5.9	191	2	Q2VGT6_PETMA	Q2vgt6 petromyzon
839	189.5	6.0	880	2	Q2XY23_DROYA	Q2xy23 drosophila	912	185.5	5.9	195	2	Q2VGT9_PETMA	Q2vgt9 petromyzon
840	189	6.0	132	2	Q2VGP2_PETMA	Q2vgp2 eptatretus	913	185.5	5.9	251	2	Q2YE24_EPTST	Q2ye24 eptatretus
841	189	6.0	298	2	Q32QU2_EPTST	Q32qu2 eptatretus	914	185.5	5.9	369	2	Q4T3M1_TETNG	Q4t3m1 tetraodon n
842	189	6.0	369	1	PGS1_MOUSE	P28653 mus musculus	915	185.5	5.9	466	2	Q661W3_XENLA	Q661w3 xenopus lae
843	189	6.0	369	1	PGS1_RAT	P47853 rattus norv	916	185.5	5.9	795	2	Q297R4_DROPS	Q297r4 drosophila
844	189	6.0	369	1	Q3TNY9_MOUSE	Q3tny9 m 15 days e	917	185.5	5.9	953	2	Q6MF87_PARUW	Q6mf87 parachlamyd
845	189	6.0	627	2	Q4TSR5_TETNG	Q4tsr5 tetraodon n	918	185	5.9	254	2	Q4S4N7_TETNG	Q4s4n7 tetraodon n
846	189	6.0	760	2	Q4QGR1_LEIMA	Q4qgr1 leishmania	919	185	5.9	323	2	Q3R2R1_EPTBU	Q3r2r1 eptatretus
847	189	6.0	839	2	Q9SN46_ARATH	Q9sn46 arabidopsis	920	185	5.9	389	2	Q6BPB5_BRARE	Q6bpb5 brachydanio
848	189	6.0	1392	2	Q9VAD1_DROME	Q9vad1 drosophila	921	185	5.9	512	2	Q6PEZ8_HUMAN	Q6pez8 homo sapien
849	189	6.0	4311	2	Q7YQK5_CANFA	Q7yqk5 canis famil	922	185	5.9	603	1	LRC40_CHICK	Q52ln0 gallus gall
850	188.5	6.0	348	2	Q32QV7_EPTST	Q32qv7 eptatretus	923	184.5	5.9	257	2	Q4GLL5_EPTBU	Q4gl15 eptatretus
851	188.5	6.0	369	2	Q6GM15_BRARE	Q6gm15 brachydanio	924	184.5	5.9	259	2	Q2YE09_EPTST	Q2ye09 eptatretus
852	188.5	6.0	370	2	Q1LXA7_BRARE	Q1lxa7 brachydanio	925	184.5	5.9	270	2	Q4KP09_LAMAP	Q4kp09 lampetra ap
853	188.5	6.0	370	2	Q5O4E0_BRARE	Q5o4e0 brachydanio	926	184.5	5.9	608	2	Q17FY2_AEDAE	Q17fy2 aedes aegyp
854	188.5	6.0	410	2	Q9DDZ7_PETMA	Q9ddz7 petromyzon	927	184.5	5.9	724	2	Q5XWB9_HORSE	Q5xwb9 equus cabal
855	188.5	6.0	433	2	Q5SYH5_MOUSE	Q5syh5 mus musculus	928	184.5	5.9	799	2	Q9V964_DROME	Q9v964 drosophila
856	188.5	6.0	440	1	OMGP_MOUSE	Q63912 mus musculus	929	184.5	5.9	839	2	Q69ZV6_MOUSE	Q69zv6 mus musculus
857	188.5	6.0	440	2	Q3UVV3_MOUSE	Q3uvv3 mus musculus	930	184.5	5.9	841	2	Q5FAK7_PIG	Q5fak7 sus scrofa
858	188.5	6.0	538	2	Q5ZBW0_ORYSA	Q5zbw0 oryza sativ	931	184.5	5.9	841	2	Q2TNK4_PIG	Q2tnk4 sus scrofa
859	188.5	6.0	655	2	Q4SBU9_TETNG	Q4sbu9 tetraodon n	932	184.5	5.9	843	1	TLR4_HORSE	Q9mwv3 equus cabal
860	188.5	6.0	677	2	Q3KR19_HUMAN	Q3kr19 homo sapien	933	184.5	5.9	957	1	SLIK5_MOUSE	Q81ob7 mus musculus
861	188	6.0	218	2	Q2VGY9_PETMA	Q2vgy9 petromyzon	934	184.5	5.9	1007	2	Q6SXS3_ORYSA	Q6sxs3 oryza sativ
862	188	6.0	334	2	Q32QR1_EPTST	Q32qr1 eptatretus	935	184.5	5.9	1046	2	Q5GQ97_CHICK	Q5gq97 gallus gall
863	188	6.0	368	2	Q53HU6_HUMAN	Q53hu6 homo sapien	936	184.5	5.9	1214	2	Q69JN6_ORYSA	Q69jn6 oryza sativ
864	188	6.0	369	1	PGS1_CANFA	Q02678 canis famil	937	184	5.9	187	2	Q6S4M5_PETMA	Q6s4m5 petromyzon
865	188	6.0	369	2	Q3UXK8_MOUSE	Q3uxk8 mus musculus	938	184	5.9	192	2	Q2VGJ6_PETMA	Q2vgj6 petromyzon
866	188	6.0	369	2	Q7TMM3_MOUSE	Q7tmm3 mus musculus	939	184	5.9	253	2	Q6S4K5_PETMA	Q6s4k5 petromyzon
867	188	6.0	522	1	LRTM1_MOUSE	Q8k377 mus musculus	940	184	5.9	263	2	Q6S4K7_PETMA	Q6s4k7 petromyzon
868	188	6.0	626	2	Q4SE92_TETNG	Q4se92 tetraodon n	941	184	5.9	274	2	Q4GLM0_EPTBU	Q4glm0 eptatretus
869	188	6.0	818	2	Q5ZIH8_CHICK	Q5zih8 gallus gall	942	184	5.9	291	2	Q4RFP21_TETNG	Q4rf21 tetraodon n
870	187.5	6.0	195	2	Q2VGR5_PETMA	Q2vgr5 petromyzon	943	184	5.9	368	1	PGS1_HUMAN	P21810 homo sapien
871	187.5	6.0	229	2	Q4G1L0_EPTBU	Q4g1l0 eptatretus	944	184	5.9	369	2	Q53F14_HUMAN	Q53f14 homo sapien
872	187.5	6.0	310	2	Q9DDZ8_PETMA	Q9ddz8 petromyzon	945	184	5.9	369	2	Q3TAP9_MOUSE	Q3tap9 mus musculus
873	187.5	6.0	350	1	TSK_XENTR	Q5m789 xenopus tro	946	184	5.9	473	2	Q7QF76_ANOGA	Q7qf76 anopheles g
874	187.5	6.0	363	2	Q9HSG9_HUMAN	Q9hsg9 homo sapien	947	184	5.9	543	2	Q4RGC6_TETNG	Q4rgc6 tetraodon n
875	187.5	6.0	425	2	Q9VGH2_DROME	Q9vgh2 drosophila	948	184	5.9	552	2	Q6K6X6_ORYSA	Q6k6x6 oryza sativ
876	187.5	6.0	601	1	LRC40_BRARE	Q7bxw3 brachydanio	949	184	5.9	565	2	Q7RJD0_ANOGA	Q7rjd0 anopheles g
877	187.5	6.0	861	2	Q4ZJ82_CHICK	Q4zj82 gallus gall	950	184	5.9	837	1	SLIK4_MOUSE	Q81ob8 mus musculus
878	187.5	6.0	885	2	Q2XY22_DROYA	Q2xy22 drosophila	951	184	5.9	1058	2	Q3WNF2_BOVIN	Q3wnf2 bos taurus
879	187	6.0	260	2	Q4G1K7_EPTST	Q4g1k7 eptatretus	952	183.5	5.9	187	2	Q6S4F6_PETMA	Q6s4f6 petromyzon
880	187	6.0	262	2	Q4G1K0_EPTST	Q4g1k0 eptatretus	953	183.5	5.9	287	2	Q9W2B9_DROME	Q9w2b9 drosophila
881	187	6.0	324	2	Q1E979_EPTST	Q1e979 eptatretus	954	183.5	5.9	292	2	Q6NYE6_BRARE	Q6ny6 brachydanio
882	187	6.0	592	2	Q61PQ4_CAER	Q61pq4 caenorhabdi	955	183.5	5.9	652	2	Q7Q696_ANOGA	Q7q696 anopheles g
883	187	6.0	615	2	Q9VZ84_DROME	Q9vz84 drosophila	956	183.5	5.9	727	2	Q6A0E8_MOUSE	Q6a0e8 mus musculus
884	187	6.0	735	2	Q6E114_MOUSE	Q6e114 mus musculus	957	183.5	5.9	795	1	TLR1_MOUSE	Q9epq1 mus musculus
885	187	6.0	807	2	Q16TW7_AEDAE	Q16tw7 aedes aegyp	958	183.5	5.9	824	2	Q5GGX1_PIG	Q5ggx1 sus scrofa
886	187	6.0	818	2	Q5WA51_CHICK	Q5wa51 gallus gall	959	183.5	5.9	841	1	TLR4_PIG	Q68y56 sus scrofa
887	187	6.0	1741	2	Q5LJU2_DROME	Q5lju2 drosophila	960	183.5	5.9	841	2	Q401C7_PIG	Q401c7 sus scrofa
888	186.5	5.9	193	2	Q2VHC4_PETMA	Q2vhc4 petromyzon	961	183.5	5.9	864	2	Q2XY30_DROSI	Q2xy30 drosophila
889	186.5	5.9	323	2	Q32QV0_EPTST	Q32qv0 eptatretus	962	183.5	5.9	864	2	Q2XY31_DROSI	Q2xy31 drosophila
890	186.5	5.9	368	1	PGS1_XENLA	Q9ib75 xenopus lae	963	183.5	5.9	867	2	Q2XY27_DROBR	Q2xy27 drosophila
891	186.5	5.9	521	2	Q72U34_LEPIC	Q72u34 leptospira	964	183.5	5.9	871	2	Q2XY28_DROYA	Q2xy28 drosophila
892	186.5	5.9	536	2	Q1EGJ9_FUGRU	Q1egj9 fugu rubrip	965	183.5	5.9	871	2	Q2XY29_DROYA	Q2xy29 drosophila
893	186.5	5.9	639	2	Q5VZ17_HUMAN	Q5vz17 homo sapien	966	183.5	5.9	1059	2	Q5ZJD0_CHICK	Q5zjd0 gallus gall
894	186.5	5.9	799	2	Q5VZ18_HUMAN	Q5vz18 homo sapien	967	183.5	5.9	1322	2	Q2M1B0_DROPS	Q2m1b0 drosophila
895	186.5	5.9	839	1	TLR4_HUMAN	Q00206 homo sapien	968	183.5	5.9	1337	1	LRC7_HUMAN	Q96nw7 homo sapien
896	186.5	5.9	839	1	TLR4_PANPA	Q9vzt0 pan paniscu	969	183	5.8	432	2	Q8BU09_MOUSE	Q8bu09 mus musculus
897	186.5	5.9	839	1	Q5VZ19_HUMAN	Q5vz19 homo sapien	970	183	5.8	540	2	Q9VU53_DROME	Q9vu53 drosophila
898	186	5.9	216	2	Q2VGR1_PETMA	Q2vgr1 petromyzon	971	183	5.8	568	2	Q6P3Y9_MOUSE	Q6p3y9 mus musculus
899	186	5.9	218	2	Q2VGR4_PETMA	Q2vgr4 petromyzon	972	183	5.8	662	1	LRC32_HUMAN	Q14332 homo sapien
900	186	5.9	273	2	Q6E4B4_PETMA	Q6e4b4 petromyzon	973	183	5.8	664	2	Q17ZT81_ONCWY	Q17zt81 oncorhynch
901	186	5.9	368	2	Q5RAY4_PONPY	Q5ray4 pongo pygma	974	183	5.8	673	2	Q17GD6_AEDAE	Q17gd6 aedes aegyp
902	186	5.9	440	1	OMGP_HUMAN	P23515 homo sapien	975	183	5.8	972	2	Q5ZU34_CHICK	Q5z3j4 gallus gall
903	186	5.9	440	2	Q53HB8_HUMAN	Q53hb8 homo sapien	976	182.5	5.8	187	2	Q6S4G7_PETMA	Q6s4g7 petromyzon
904	186	5.9	517	2	Q299N9_DROPS	Q299n9 drosophila	977	182.5	5.8	187	2	Q6S4G1_PETMA	Q6s4g1 petromyzon
905	186	5.9	552	2	Q9VT44_DROME	Q9vt44 drosophila	978	182.5	5.8	219	2	Q2VGV7_PETMA	Q2vgv7 petromyzon
906	186	5.9	623	1	LRC21_HUMAN	Q9p2v4 homo sapien	979	182.5	5.8	257	2	Q4G1L8_EPTBU	Q4gl18 eptatretus
907	186	5.9	1029	1	TLR9_BOVIN	Q512m5 bos taurus	980	182.5	5.8	261	2	Q2YE27_EPTBU	Q2ye27 eptatretus

981	182.5	5.8	298	2	Q32QV7_EPTBU	Q32qv7 eptaretus	1054	179.5	5.7	585	2	Q61GX3_CABBR	O61gx3 caenorhabdi
982	182.5	5.8	379	1	ASPN_HUMAN	Q9bxx1 homo sapien	1055	179.5	5.7	799	2	Q3BBY2_MACVU	Q3bbv2 macaca mupa
983	182.5	5.8	380	2	OSTBF3_HUMAN	O5tbf3 homo sapien	1056	179.5	5.7	820	2	Q5R3F8_HUMAN	O5r3f8 homo sapien
984	182.5	5.8	384	2	G6P528_HUMAN	G6p528 homo sapien	1057	179.5	5.7	1117	1	LRIG3_MOUSE	O6plc6 mus musculus
985	182.5	5.8	618	2	Q1L8W7_BRARE	Q1l8w7 brachydanio	1058	179.5	5.7	4283	2	Q9ERV0_RAT	Q9erv0 rattus norv
986	182.5	5.8	810	2	Q8TJ32_DROME	Q8tj32 drosophila	1059	179	5.7	192	2	Q2VH01_PETMA	Q2vh01 petromyzon
987	182.5	5.8	811	2	Q9VK54_DROME	Q9vk54 drosophila	1060	179	5.7	192	2	Q2VGC7_PETMA	Q2vgc7 petromyzon
988	182.5	5.8	828	1	TLR4_PONPY	O8spes pongo pygma	1061	179	5.7	192	2	Q2VGV8_PETMA	Q2vgv8 petromyzon
989	182.5	5.8	837	1	TLR4_GORGO	O8spes gorilla gor	1062	179	5.7	194	2	Q2VH46_PETMA	Q2vh46 petromyzon
990	182.5	5.8	864	2	Q2XY32_DROME	P2xy32 drosophila	1063	179	5.7	262	2	Q2VE11_EPTST	Q2ve11 eptaretus
991	182.5	5.8	880	2	P91643_DROME	P91643 drosophila	1064	179	5.7	273	2	Q6E488_PETMA	Q6e488 petromyzon
992	182.5	5.8	958	1	SLIK5_HUMAN	O94991 homo sapien	1065	179	5.7	314	1	LRCS52_MOUSE	Q5m8n9 mus musculus
993	182.5	5.8	958	2	O5VT81_HUMAN	O5vt81 homo sapien	1066	179	5.7	534	2	Q9VT89_DROME	Q9vt89 drosophila
994	182.5	5.8	958	2	Q4QOH1_HUMAN	O4qoh1 homo sapien	1067	179	5.7	700	2	Q9P244_HUMAN	O9p244 homo sapien
995	182.5	5.8	999	2	O17PV0_AEDAE	O17pv0 aedes aegyp	1068	179	5.7	742	2	O9BJD4_STRPU	O9bjd4 strongyloce
996	182.5	5.8	1041	2	Q3HJ14_TRIER	Q3hj14 trichodesmi	1069	179	5.7	815	2	Q17LD1_AEDAE	Q17ld1 aedes aegyp
997	182	5.8	192	2	Q2VGF9_PETMA	Q2vgf9 petromyzon	1070	179	5.7	905	1	TLR3_MOUSE	Q99mb1 mus musculus
998	182	5.8	194	2	Q2VGV0_PETMA	Q2vgv0 petromyzon	1071	179	5.7	905	2	Q499F3_MOUSE	Q499f3 mus musculus
999	182	5.8	205	2	Q4R9X7_TETNG	O4rx7 tetraodon n	1072	179	5.7	969	2	Q4LBC9_ONCMY	Q4lbc9 oncorhynch
1000	182	5.8	252	2	Q4G1I8_EPTST	O4gl18 eptaretus	1073	179	5.7	1029	1	TLR9_SHEEP	O5i2n4 ovis aries
1001	182	5.8	271	2	O6E4C4_PETMA	O6e4c4 petromyzon	1074	178.5	5.7	161	2	Q2VH51_PETMA	Q2vh51 petromyzon
1002	182	5.8	297	2	Q4RU73_TETNG	Q4ru73 tetraodon n	1075	178.5	5.7	176	2	O567L5_BRARE	O567l5 brachydanio
1003	182	5.8	319	2	Q32R34_EPTBU	Q32r34 eptaretus	1076	178.5	5.7	190	2	Q6E4D8_PETMA	Q6e4d8 petromyzon
1004	182	5.8	369	1	PGS1_BOVIN	P21809 bos taurus	1077	178.5	5.7	348	2	O5RI43_BRARE	O5ri43 brachydanio
1005	182	5.8	369	1	PGS1_SHEEP	O46390 ovis aries	1078	178.5	5.7	356	1	PGS2_COTJA	O9de68 coturnix co
1006	182	5.8	369	2	Q17OB0_BOVIN	O17ob0 bos taurus	1079	178.5	5.7	443	2	O67VV7_ORYSA	O67vv7 oryza sativ
1007	182	5.8	373	2	O5RI45_BRARE	O5ri45 brachydanio	1080	178.5	5.7	493	1	AMG01_HUMAN	O86wk6 homo sapien
1008	182	5.8	373	2	Q803T1_BRARE	Q803t1 brachydanio	1081	178.5	5.7	587	2	Q4QGJ9_LEITMA	O4qgj9 leishmania
1009	182	5.8	428	2	Q8F3F8_LEPIN	Q8f3f8 leptospira	1082	178.5	5.7	1024	1	POPC_RALSO	Q9rbs2 ralsconia s
1010	182	5.8	532	2	O96671_DROME	O96671 drosophila	1083	178.5	5.7	1063	2	O5Z666_ORYSA	O5z666 oryza sativ
1011	182	5.8	678	2	Q7Q550_ANOGA	O7q550 anopheles g	1084	178.5	5.7	1104	2	Q7XUH4_ORYSA	O7xuh4 oryza sativ
1012	182	5.8	1022	2	O8HXV0_BOVIN	O8hxv0 bos taurus	1085	178.5	5.7	1107	2	Q3MD20_ANAVY	Q3md20 anabaena va
1013	182	5.8	1029	2	O866B2_BOVIN	O866b2 bos taurus	1086	178.5	5.7	1310	1	GP125_MOUSE	O7t2t36 mus musculus
1014	181.5	5.8	180	2	O8BPJ0_MOUSE	O8bpj0 mus musculus	1087	178	5.7	187	2	O6E4H4_PETMA	O6e4h4 petromyzon
1015	181.5	5.8	185	2	Q2VGV0_PETMA	Q2vgv0 petromyzon	1088	178	5.7	192	2	Q2VH53_PETMA	Q2vh53 petromyzon
1016	181.5	5.8	191	2	Q2VH42_PETMA	Q2vh42 petromyzon	1089	178	5.7	192	2	Q2VH56_PETMA	Q2vh56 petromyzon
1017	181.5	5.8	251	2	O4G1K2_EPTST	O4glk2 eptaretus	1090	178	5.7	194	2	Q2VGE4_PETMA	Q2vge4 petromyzon
1018	181.5	5.8	259	2	O4G1J8_EPTST	O4glj8 eptaretus	1091	178	5.7	231	2	Q3TV01_MOUSE	Q3tv01 mus musculus
1019	181.5	5.8	298	2	Q32RA1_EPTBU	Q32ra1 eptaretus	1092	178	5.7	296	2	Q32QX9_EPTST	Q32qx9 eptaretus
1020	181.5	5.8	357	1	PGS2_CHICK	P28675 gallus gall	1093	178	5.7	238	2	Q32QX4_EPTST	Q32qx4 eptaretus
1021	181.5	5.8	599	2	Q7T3H6_BRARE	Q7t3h6 brachydanio	1094	178	5.7	319	2	Q32QZ3_EPTBU	Q32qz3 eptaretus
1022	181.5	5.8	670	2	O16P50_AEDAE	O16p50 aedes aegyp	1095	178	5.7	364	2	O66J59_XENIA	O66j59 xenopus lae
1023	181.5	5.8	699	2	O61PG3_CABBR	O61pg3 caenorhabdi	1096	178	5.7	391	2	O4RQ11_TETNG	O4rq11 tetraodon n
1024	181.5	5.8	1434	2	O17NJ6_AEDAE	O17nj6 aedes aegyp	1097	178	5.7	488	2	O4RXQ5_TETNG	O4rxq5 tetraodon n
1025	181.5	5.8	2160	2	O13488_MAGGR	O13488 magnaporthe	1098	178	5.7	522	1	LRTW1_HUMAN	O86ue6 homo sapien
1026	181.5	5.8	2160	2	O13328_MAGGR	O13328 magnaporthe	1099	178	5.7	578	2	O28CE3_XENTR	Q28ce3 xenopus tro
1027	181	5.8	192	2	Q2VGV4_PETMA	Q2vgv4 petromyzon	1100	178	5.7	894	2	Q9BJD6_STRPU	Q9bjd6 strongyloce
1028	181	5.8	298	2	O2YEG9_EPTST	O2yeg9 eptaretus	1101	178	5.7	1049	1	TLR7_HUMAN	Q9nyk1 homo sapien
1029	181	5.8	372	1	PGS1_HORSE	O46403 equus cabal	1102	178	5.7	1052	2	Q9Y4C4_HUMAN	Q9y4c4 homo sapien
1030	181	5.8	569	2	O7Q1F3_ANOGA	O7qi13 anopheles g	1103	178	5.7	1257	2	Q7PNF8_ANOGA	Q7pnf8 anopheles g
1031	181	5.8	1013	2	Q8LQ10_ORYSA	O8lq10 oryza sativ	1104	177.5	5.7	187	2	Q2VH41_PETMA	Q2vh41 petromyzon
1032	181	5.8	1333	2	Q7Q168_ANOGA	Q7qi68 anopheles g	1105	177.5	5.7	195	2	Q2VGD7_PETMA	Q2vgd7 petromyzon
1033	180.5	5.8	371	2	O6GLQ6_XENIA	O6glq6 xenopus lae	1106	177.5	5.7	215	2	Q2VGS6_PETMA	Q2vgs6 petromyzon
1034	180.5	5.8	385	2	O8BMW6_MOUSE	O8bmw6 mus musculus	1107	177.5	5.7	275	2	O4G1K5_EPTST	O4glk5 eptaretus
1035	180.5	5.8	441	2	O8I170_DROVI	O8i170 drosophila	1108	177.5	5.7	796	2	O4LDR7_PIG	O4ldr7 sus scrofa
1036	180.5	5.8	522	1	AMG02_PONPY	O5r7m3 pongo pygma	1109	177.5	5.7	796	2	O59H19_PIG	O59h19 sus scrofa
1037	180.5	5.8	584	2	O6PGX3_BRARE	O6pgx3 brachydanio	1110	177.5	5.7	809	2	O4RMQ1_TETNG	O4rmq1 tetraodon n
1038	180.5	5.8	821	2	Q96PY3_HUMAN	Q96py3 homo sapien	1111	177.5	5.7	1026	2	Q5SMW2_ORYSA	Q5smw2 oryza sativ
1039	180.5	5.8	859	2	Q1ZZX0_MUSMM	Q1zzx0 mus musculus	1112	177.5	5.7	1050	1	TLR7_MOUSE	P586b1 mus musculus
1040	180.5	5.8	1376	2	O16X81_AEDAE	O16x81 aedes aegyp	1113	177.5	5.7	1050	2	O548J0_MOUSE	O548j0 m toll-like
1041	180.5	5.8	1443	2	O9VJ00_DROME	O9vj00 drosophila	1114	177.5	5.7	1360	2	O7KTA0_DROME	O7kta0 drosophila
1042	180.5	5.8	1460	2	O5HZ61_XENTR	O5hz61 xenopus tro	1115	177.5	5.7	2300	1	CYAA_NEUCR	Q01631 neuospora
1043	180	5.7	192	2	Q2VH29_PETMA	Q2vh29 petromyzon	1116	177.5	5.7	2493	2	CYAA_USTMA	P49606 utiilago ma
1044	180	5.7	250	2	O4GIM2_EPTBU	O4gim2 eptaretus	1117	177.5	5.7	2493	2	Q4P3T1_USTMA	Q4p3t1 utiilago ma
1045	180	5.7	436	2	Q29FB4_DROPS	Q29fb4 drosophila	1118	177	5.6	187	2	O6E4H5_PETMA	Q6e4h5 petromyzon
1046	180	5.7	522	1	LRTM1_PONPY	Q5r6b1 pongo pygma	1119	177	5.6	192	2	Q2VH26_PETMA	Q2vh26 petromyzon
1047	180	5.7	817	2	O9VS84_DROME	O9vs84 drosophila	1120	177	5.6	192	2	Q2VGO0_PETMA	Q2vgo0 petromyzon
1048	180	5.7	817	2	O86P15_DROME	O86p15 drosophila	1121	177	5.6	192	2	Q2VGR6_PETMA	Q2vgr6 petromyzon
1049	180	5.7	843	2	O7ZTG5_CHICK	O7zts5 gallus gall	1122	177	5.6	192	2	Q2VGM2_PETMA	Q2vgm2 petromyzon
1050	180	5.7	869	2	Q4S0C1_TETNG	Q4s0c1 tetraodon n	1123	177	5.6	192	2	Q2VH28_PETMA	Q2vh28 petromyzon
1051	179.5	5.7	179	5.8	Q2VGI7_PETMA	Q2vgi7 petromyzon	1124	177	5.6	334	2	O4SBU8_TETNG	Q4sbu8 tetraodon n
1052	179.5	5.7	187	2	O6E4D6_PETMA	O6e4d6 petromyzon	1125	177	5.6	343	1	LUM_COTJA	Q9de67 coturnix co
1053	179.5	5.7	195	2	Q2VGP4_PETMA	Q2vgp4 petromyzon	1126	177	5.6	615	2	Q29EA2_DROPS	Q29ea2 drosophila

1127	177	5.6	662	1	LRC32_PONPY	05rf01_pongo pygma	1200	174	5.6	651	2	04JQ02_XENLA	04jq02_xenopus lae
1128	177	5.6	666	2	Q7Q2W6_ANOGA	Q7q2w6_anopheles g	1201	174	5.6	859	1	TLR5_MOUSE	Q9j1f7_mus musculus
1129	177	5.6	670	2	Q5FW85_MOUSE	Q5fw85_m extracell	1202	174	5.6	913	2	Q3KUR8_ONCMY	Q3kur8_oncorhynch
1130	177	5.6	1370	2	Q58NA4_APIME	Q58na4_apis mellif	1203	174	5.6	951	1	LGR4_RAT	Q9z2h4_rattus norv
1131	176.5	5.6	185	2	Q2VG95_PETMA	Q2vg95_petryomzon	1204	174	5.6	1361	1	Q17FX0_AEDAE	Q17fx0_aedes aegyp
1132	176.5	5.6	187	2	Q6E4M0_PETMA	Q6e4m0_petryomzon	1205	174	5.6	1367	2	Q1RMC9_HUMAN	Q1rmc9_homo sapien
1133	176.5	5.6	195	2	Q2VGT9_PETMA	Q2vgt9_petryomzon	1206	174	5.6	1371	2	Q1RMD0_HUMAN	Q1rmd0_homo sapien
1134	176.5	5.6	322	2	Q32R02_EPTBU	Q32r02_eptaretus	1207	173.5	5.5	161	2	Q2VH22_PETMA	Q2vh22_petryomzon
1135	176.5	5.6	520	2	Q5VR46_ORYSA	Q5vr46_oryza sativ	1208	173.5	5.5	261	2	Q5MR11_HUMAN	Q5mr11_homo sapien
1136	176.5	5.6	522	1	AMGO2_HUMAN	Q86s72_homo sapien	1209	173.5	5.5	337	2	Q4RJX0_TETNG	Q4rjx0_tetradodon n
1137	176.5	5.6	522	2	Q4VPB6_HUMAN	Q4vpb6_homo sapien	1210	173.5	5.5	353	2	Q640B1_XENTR	Q640b1_xenopus tro
1138	176.5	5.6	628	2	Q7PV26_ANOGA	Q7pv26_anopheles g	1211	173.5	5.5	364	2	Q6GNX8_XENLA	Q6gnx8_xenopus lae
1139	176.5	5.6	856	2	Q59H17_PIG	Q59h17_sus scrofa	1212	173.5	5.5	421	1	OMD_HUMAN	Q999b3_homo sapien
1140	176.5	5.6	905	2	Q4SBD4_TETNG	Q4sbd4_tetradodon n	1213	173.5	5.5	421	2	Q5TEF4_HUMAN	Q5tbf4_homo sapien
1141	176.5	5.6	1495	1	LRRCT7_RAT	P70587_rattus norv	1214	173.5	5.5	440	2	Q7TQ25_RAT	Q7tq25_rattus norv
1142	176	5.6	220	2	Q4VH09_PETMA	Q2vh09_petryomzon	1215	173.5	5.5	537	1	LGI4_MOUSE	Q8kl61_mus musculus
1143	176	5.6	249	2	Q4SUN4_TETNG	Q4sun4_tetradodon n	1216	173.5	5.5	537	2	Q3UYI9_MOUSE	Q3uyi9_mus musculus
1144	176	5.6	503	2	Q8LJ87_ORYSA	Q8lj87_oryza sativ	1217	173.5	5.5	727	2	Q6GV21_BOVIN	Q6gv21_bos taurus
1145	176	5.6	623	2	Q95R21_DROME	Q95r21_drosophila	1218	173.5	5.5	806	2	Q7TPC5_MOUSE	Q7tpc5_mus musculus
1146	176	5.6	862	2	Q5GR02_CHICK	Q5gr02_gallus gall	1219	173.5	5.5	826	1	TLR4_PAPAN	Q9t8p2_papio anubi
1147	176	5.6	904	2	Q5TU59_BOVIN	Q5tj59_bos taurus	1220	173.5	5.5	884	2	Q5H720_FUGRU	Q5h720_fugu rubrip
1148	176	5.6	905	2	Q5TU58_BOVIN	Q5tj58_bos taurus	1221	173.5	5.5	1167	2	Q16XG0_AEDAE	Q16xg0_aedes aegyp
1149	176	5.6	906	2	Q4SR20_TETNG	Q4sr20_tetradodon n	1222	173.5	5.5	1681	2	Q299Y2_DROPS	Q299y2_drosophila
1150	176	5.6	913	2	Q1PA38_ONCMY	Q1pa38_oncorhynch	1223	173	5.5	1681	2	Q2VCK8_PETMA	Q2vck8_petryomzon
1151	176	5.6	1032	1	TLR9_CANFA	Q5i2m8_canis famil	1224	173	5.5	192	2	Q2VHA2_PETMA	Q2vha2_petryomzon
1152	176	5.6	1257	1	Q9VKZ8_DROME	Q9vkz8_drosophila	1225	173	5.5	192	2	Q2VCG5_PETMA	Q2vgs5_petryomzon
1153	176	5.6	1412	1	LAP2_HUMAN	Q96rt1_homo sapien	1226	173	5.5	194	2	Q2VHC8_PETMA	Q2vnc8_petryomzon
1154	175.5	5.6	167	2	Q2VGH3_PETMA	Q2vgv3_petryomzon	1227	173	5.5	252	2	Q4G114_EPTST	Q4g114_eptaretus
1155	175.5	5.6	185	2	Q2VGH3_PETMA	Q2vgv3_petryomzon	1228	173	5.5	269	2	Q6E4C2_PETMA	Q6e4c2_petryomzon
1156	175.5	5.6	251	2	Q2YE03_EPTST	Q2ye03_eptaretus	1229	173	5.5	360	1	PGS2_HORSE	Q46542_equus cabal
1157	175.5	5.6	272	2	Q4KP14_9PTTR	Q4kp14_ichtthyomyzo	1230	173	5.5	470	2	Q9V354_DROME	Q9v354_drosophila
1158	175.5	5.6	324	2	Q32R05_EPTBU	Q32r05_eptaretus	1231	173	5.5	539	2	Q503F6_BRARE	Q503f6_brachydania
1159	175.5	5.6	384	2	Q4T0V4_TETNG	Q4t0v4_tetradodon n	1232	173	5.5	664	2	Q5UT54_SAUSA	Q5ut54_salmo salar
1160	175.5	5.6	440	2	Q7TNN3_RAT	Q7tnc3_rattus norv	1233	173	5.5	853	2	Q8CB40_MOUSE	Q8cb40_mus musculus
1161	175.5	5.6	492	1	AMGO1_MOUSE	Q80z68_mus musculus	1234	173	5.5	892	1	GLHR_AKTEF	Q466h0_methanosarc
1162	175.5	5.6	816	2	Q29L68_DROPS	Q29l68_drosophila	1235	173	5.5	925	1	Q7Q0C5_ANOGA	Q7q0c5_anopheles g
1163	175.5	5.6	841	2	Q2V898_BOSTR	Q2v898_boselaphus	1236	173	5.5	1459	2	Q8WRE4_ANOGA	Q8wr44_anopheles g
1164	175.5	5.6	1017	2	Q5H718_FUGRU	Q5h718_fugu rubrip	1237	173	5.5	1459	2	Q2VHB2_PETMA	Q2vnb2_petryomzon
1165	175.5	5.6	1490	1	LRRCT7_MOUSE	Q80t67_mus musculus	1238	172.5	5.5	161	2	Q2VGH1_PETMA	Q2vgh1_petryomzon
1166	175.5	5.6	1731	2	Q4S0D3_TETNG	Q4s0d3_tetradodon n	1239	172.5	5.5	161	2	Q6E4E2_PETMA	Q6e4e2_petryomzon
1167	175	5.6	168	2	Q2VHC0_PETMA	Q2vnc0_petryomzon	1240	172.5	5.5	163	2	Q2VHC2_PETMA	Q2vnc2_petryomzon
1168	175	5.6	192	2	Q2VH74_PETMA	Q2vh74_petryomzon	1241	172.5	5.5	171	2	Q2YE13_EPTST	Q2ye13_eptaretus
1169	175	5.6	192	2	Q2VGH6_PETMA	Q2vgk6_petryomzon	1242	172.5	5.5	237	2	Q2YE22_EPTST	Q2ye22_eptaretus
1170	175	5.6	252	2	Q4GIJ2_EPTST	Q4gi12_eptaretus	1243	172.5	5.5	259	2	Q2YE22_EPTST	Q2ye22_eptaretus
1171	175	5.6	297	2	Q32Q20_EPTBU	Q32qz0_eptaretus	1244	172.5	5.5	353	1	KERA_CHICK	Q422d5_gallus gall
1172	175	5.6	323	2	Q32R31_EPTBU	Q32r31_eptaretus	1245	172.5	5.5	353	1	KERA_COTJA	Q9d666_coturnix co
1173	175	5.6	343	1	LUM_CHICK	P51890_gallus gall	1246	172.5	5.5	359	1	PGS2_HUMAN	P07585_homo sapien
1174	175	5.6	474	2	Q29XV6_DROPS	Q290x6_drosophila	1247	172.5	5.5	359	1	PGS2_PANTR	Q5r1v9_pan troglod
1175	175	5.6	510	2	Q9BGV6_MACFA	Q9bgv6_macaca fasc	1248	172.5	5.5	359	2	Q6FHT0_HUMAN	Q6fht0_homo sapien
1176	175	5.6	512	2	Q17F18_AEDAE	Q17f18_aedes aegyp	1249	172.5	5.5	378	2	Q5R294_DROSI	Q5r294_drosophila
1177	175	5.6	905	2	Q3TW31_MOUSE	Q3tm31_mus musculus	1250	172.5	5.5	739	2	Q60NV9_CABBR	Q60nv9_caenorhabdi
1178	175	5.6	941	2	Q5H722_FUGRU	Q5h722_fugu rubrip	1251	172.5	5.5	823	2	Q68FM6_MOUSE	Q68fm6_mus musculus
1179	175	5.6	973	2	Q6KCC7_ONCMY	Q6kcc7_oncorhynch	1252	172.5	5.5	823	2	Q8CCW8_MOUSE	Q8ccw8_mus musculus
1180	175	5.6	1031	2	Q2EEV0_HORSE	Q2eev0_equus cabal	1253	172.5	5.5	1851	1	LAP4_DROME	Q7kry7_drosophila
1181	175	5.6	1137	2	Q7QHH1_ANOGA	Q7qhh1_anopheles g	1254	172.5	5.5	4256	2	Q8MJF3_CANFA	Q8mjf3_canis famil
1182	174.5	5.6	1130	2	Q6E4E5_PETMA	Q6e4e5_petryomzon	1255	172	5.5	339	2	Q4S068_TETNG	Q4s068_tetradodon n
1183	174.5	5.6	191	2	Q2VGI5_PETMA	Q2vgi5_petryomzon	1256	172	5.5	347	1	TSK_BRARE	Q58a48_brachydania
1184	174.5	5.6	193	2	Q2VGD0_PETMA	Q2vgd0_petryomzon	1257	172	5.5	411	2	Q4S9P3_TETNG	Q4s9p3_tetradodon n
1185	174.5	5.6	440	2	Q4J5V4_AZOVI	Q4j5v4_azotobacter	1258	172	5.5	577	2	Q8N3K5_HUMAN	Q8n3k5_homo sapien
1186	174.5	5.6	512	2	Q9CQ76_MOUSE	Q9cq76_m_8 days em	1259	172	5.5	904	2	Q1G1A3_HUBBU	Q1g1a3_bubalus bub
1187	174.5	5.6	567	2	Q4SLI0_TETNG	Q4sl10_tetradodon n	1260	172	5.5	1134	2	Q65510_ARATH	Q65510_arabidopsis
1188	174.5	5.6	602	1	LRC40_MOUSE	Q9cr68_mus musculus	1261	172	5.5	1693	2	Q2VGH0_GIBZE	Q2vgh0_petryomzon
1189	174.5	5.6	605	1	LRC40_XENLA	Q6gpj5_xenopus lae	1262	171.5	5.5	171	2	Q2VGH1_PETMA	Q2vgh1_petryomzon
1190	174.5	5.6	795	1	TLR6_MOUSE	Q9epw9_mus musculus	1263	171.5	5.5	193	2	Q2VHD1_PETMA	Q2vhd1_petryomzon
1191	174.5	5.6	806	2	Q3UVF8_MOUSE	Q3uvf8_mus musculus	1264	171.5	5.5	195	2	Q2VH57_PETMA	Q2vh57_petryomzon
1192	174.5	5.6	1020	2	Q5ZED4_ORYSA	Q5zed4_oryza sativ	1265	171.5	5.5	378	2	Q9V900_DROME	Q9v900_drosophila
1193	174.5	5.6	1060	2	Q6ZGN3_ORYSA	Q6zgm3_oryza sativ	1266	171.5	5.5	605	1	LRC40_XENTR	Q5m844_xenopus tro
1194	174	5.6	194	2	Q2VGH3_PETMA	Q2vgv3_petryomzon	1267	171.5	5.5	683	1	LRC40_HUMAN	Q75427_homo sapien
1195	174	5.6	196	2	Q2VGH0_PETMA	Q2vgf0_petryomzon	1268	171.5	5.5	791	2	Q2L8H0_LISMO	Q2l8h0_listeria mo
1196	174	5.6	299	2	Q32R28_EPTBU	Q32r28_eptaretus	1269	171.5	5.5	858	1	LRC8D_RAT	Q5u308_rattus norv
1197	174	5.6	490	2	Q4RY15_TETNG	Q4ry15_tetradodon n	1270	171.5	5.5	858	1	TLR5_HUMAN	Q60602_homo sapien
1198	174	5.6	535	2	Q8RX50_BRANI	Q8rx50_brassica ni	1271	171.5	5.5	858	2	Q32MI3_HUMAN	Q32mi3_homo sapien
1199	174	5.6	544	2	Q7Q2W5_ANOGA	Q7q2w5_anopheles g	1272	171.5	5.5	858	2	Q32MI2_HUMAN	Q32mi2_homo sapien

1273	171.5	5.5	859	1	LRC8D_MOUSE	Q8bgr2	mus musculus	1346	168.5	5.4	343	2	Q501S3_BRARE	Q501s3 brachydanio
1274	171.5	5.5	859	2	Q3Ti70_MOUSE	Q3ti70	mus musculus	1347	168.5	5.4	353	2	Q7SYS8_XENLA	Q7sys8 xenopus lae
1275	171.5	5.5	1589	2	Q9UUG9_METAN	Q9uug9	metarhizium	1348	168.5	5.4	363	2	Q8C8A7_MOUSE	Q8c8a7 mus musculus
1276	171	5.5	168	2	Q2VHR6_PETWA	Q2vhr6	petromyzon	1349	168.5	5.4	366	2	Q3UGP9_MOUSE	Q3ugp9 mus musculus
1277	171	5.5	192	2	Q2VGS1_PETWA	Q2vgs1	petromyzon	1350	168.5	5.4	378	2	Q5R264_DROSE	Q5r264 drosophila
1278	171	5.5	194	2	Q2VGS3_PETWA	Q2vgs3	petromyzon	1351	168.5	5.4	619	2	Q6R8K0_ORYSA	Q6r8k0 oryza sativ
1279	171	5.5	299	2	Q32Q27_EPTBU	Q32q27	eptatretus	1352	168.5	5.4	685	2	Q6T545_LISMO	Q6t545 listeria mo
1280	171	5.5	354	2	Q3TSV1_MOUSE	Q3tsv1	mus musculus	1353	168.5	5.4	694	2	Q61P91_CAEBR	Q61p91 caenorhabdi
1281	171	5.5	360	1	PGS2_PIG	Q9xkd9	sus scrofa	1354	168.5	5.4	728	2	Q6T546_LISMO	Q6t546 listeria mo
1282	171	5.5	360	2	Q6DV11_GECJA	Q6dv11	gecko japon	1355	168.5	5.4	744	2	Q8KTF6_LISMO	Q8ktf6 listeria mo
1283	171	5.5	469	2	Q3URB9_MOUSE	Q3urb9	mus musculus	1356	168.5	5.4	791	2	Q2L8H6_LISMO	Q2l8h6 listeria mo
1284	171	5.5	512	2	Q17F19_AEDAE	Q17f19	aedes aegypt	1357	168.5	5.4	800	2	Q4EQX8_LISMO	Q4eqx8 listeria mo
1285	171	5.5	517	2	Q17K69_AEDAE	Q17k69	aedes aegypt	1358	168.5	5.4	907	1	LGR5_MOUSE	Q921p4 mus musculus
1286	171	5.5	643	2	Q5O2J4_BRARE	P58727	brachydanio	1359	168.5	5.4	1036	2	Q9FN37_ARATH	Q9fn37 arabidopsis
1287	171	5.5	833	1	TLR4_FELCA	Q58727	felis silve	1360	168.5	5.4	1360	2	Q9ND11_DROSE	Q9nd11 drosophila
1288	171	5.5	976	2	Q3VIN1_MOUSE	Q3vin1	mus musculus	1361	168.5	5.4	1724	2	Q4H4B6_BRARE	Q4h4b6 brachydanio
1289	171	5.5	976	2	Q3TAN2_MOUSE	Q3tan2	mus musculus	1362	168.5	5.4	3201	2	Q2QBE0_9ALPH	Q2qbe0 cercopithec
1290	171	5.5	1091	2	Q17L59_AEDAE	Q17l59	aedes aegypt	1363	168.5	5.4	351	2	Q32N68_XENLA	Q32n68 xenopus lae
1291	171	5.5	1317	2	Q5TUS9_ANOGA	Q5tus9	anopheles g	1364	168.5	5.4	351	2	Q65YW8_XENLA	Q65yw8 xenopus lae
1292	170.5	5.4	185	2	Q2VGH0_PETWA	Q2vgh0	petromyzon	1365	168.5	5.4	369	2	Q28X02_DROPS	Q28x02 drosophila
1293	170.5	5.4	246	2	Q6EAJ1_PETWA	Q6eaj1	petromyzon	1366	168.5	5.4	402	2	Q72U35_LEPIC	Q72u35 leptospira
1294	170.5	5.4	359	2	Q4RSD2_MACFA	Q4rsd2	macaca fasc	1367	168.5	5.4	539	2	Q16K00_AEDAE	Q16k00 aedes aegypt
1295	170.5	5.4	373	1	ASPN_MOUSE	Q99mq4	mus musculus	1368	168.5	5.4	773	2	Q5NE35_LISMO	Q5ne35 listeria mo
1296	170.5	5.4	741	2	Q8KTF7_LISMO	Q8ktf7	listeria mo	1369	168.5	5.4	951	1	LGR4_HUMAN	Q8gvw0 homo sapien
1297	170.5	5.4	761	2	Q3XNG0_9PROT	Q3xng0	magnetococc	1370	168.5	5.4	977	2	Q8GVW0_ORYSA	Q8gtt00 sus scrofa
1298	170.5	5.4	794	2	Q2L8H9_LISMO	Q2l8h9	listeria mo	1371	168.5	5.4	1050	2	Q2L4T3_CANFA	Q2l4t3 canis famil
1299	170.5	5.4	1031	1	TLR9_FELCA	Q5i2m7	felis silve	1372	167.5	5.3	147	2	Q9TT00_PIG	Q9tt00 sus scrofa
1300	170.5	5.4	2145	1	CYAN_PODAN	Q01513	podocypora a	1373	167.5	5.3	171	2	Q2VHCL_PETWA	Q2vhcl petromyzon
1301	170	5.4	187	2	Q6E4D9_PETWA	Q6e4d9	petromyzon	1374	167.5	5.3	185	2	Q2VGV4_PETWA	Q2vgv4 petromyzon
1302	170	5.4	192	2	Q2VGM4_PETWA	Q2vgm4	petromyzon	1375	167.5	5.3	351	1	KERA_MOUSE	Q35367 mus musculus
1303	170	5.4	192	2	Q2VH20_PETWA	Q2vh20	petromyzon	1376	167.5	5.3	360	1	PGS2_SHEEP	Q9tte2 ovis aries
1304	170	5.4	192	2	Q2VGS2_PETWA	Q2vgs2	petromyzon	1377	167.5	5.3	378	2	Q72U36_LEPIC	Q72u36 leptospira
1305	170	5.4	192	2	Q2VGI9_PETWA	Q2vgi9	petromyzon	1378	167.5	5.3	396	2	Q8C3D9_MOUSE	Q8c3d9 mus musculus
1306	170	5.4	364	1	LRCI39_MOUSE	Q8bzt5	mus musculus	1379	167.5	5.3	422	1	QMD_BOVIN	Q7742 bos taurus
1307	170	5.4	415	2	Q295B8_DROPS	Q295b8	drosophila	1380	167.5	5.3	550	2	Q2QXR6_ORYSA	Q2qx66 oryza sativ
1308	170	5.4	473	2	Q3TSQ3_MOUSE	Q3tsq3	mus musculus	1381	167.5	5.3	568	2	Q16M66_AEDAE	Q16m66 aedes aegypt
1309	170	5.4	545	2	Q1EGK2_FUGRU	Q1egk2	fugu rubrip	1382	167.5	5.3	694	2	Q4RYL2_TETNG	Q4ryl2 tetraodon n
1310	170	5.4	572	2	Q4QGJ6_LEIMA	Q4qgj6	leishmania	1383	167.5	5.3	907	2	Q3VIL2_MOUSE	Q3vil2 mus musculus
1311	170	5.4	883	2	Q4VAM0_HUMAN	Q4van0	homo sapien	1384	167.5	5.3	917	2	Q75GM9_ORYSA	Q75gm9 oryza sativ
1312	170	5.4	907	1	LGR5_HUMAN	Q75473	homo sapien	1385	167.5	5.3	1174	2	Q25AQ0_ORYSA	Q25aq0 oryza sativ
1313	170	5.4	907	2	Q4VAM2_HUMAN	Q4van2	homo sapien	1386	167.5	5.3	1174	2	Q7XS37_ORYSA	Q7xs37 oryza sativ
1314	170	5.4	1024	2	Q84I66_RALSO	Q84i66	ralatonia s	1387	167.5	5.3	1225	2	Q16V17_AEDAE	Q16v17 aedes aegypt
1315	170	5.4	1032	2	Q59ER8_HUMAN	Q59er8	homo sapien	1388	167.5	5.3	168	2	Q2VGM8_PETWA	Q2vgm8 petromyzon
1316	169.5	5.4	167	2	Q2VGL5_PETWA	Q2vgl5	petromyzon	1389	167.5	5.3	262	2	Q2YE18_EPTST	Q2ye18 eptatretus
1317	169.5	5.4	173	2	Q2VGD2_PETWA	Q2vgd2	petromyzon	1390	167.5	5.3	537	2	Q6P2A4_RAT	Q6p2a4 rattus norv
1318	169.5	5.4	352	1	KERA_BOVIN	Q82702	bos taurus	1391	167.5	5.3	582	2	Q6AYI5_RAT	Q6ay15 rattus norv
1319	169.5	5.4	366	2	Q8BX06_MOUSE	Q8bx06	mus musculus	1392	167.5	5.3	633	2	Q8F3F6_LEPIN	Q8f3f6 leptospira
1320	169.5	5.4	463	2	Q2LYW7_DROPS	Q2lyw7	drosophila	1393	167.5	5.3	743	2	Q8KCF7_LISMO	Q8kcf7 listeria mo
1321	169.5	5.4	493	1	AMG01_RAT	Q80zd7	rattus norv	1394	167.5	5.3	744	2	Q8KTF4_LISMO	Q8ktf4 listeria mo
1322	169.5	5.4	651	2	Q4TRT5_TETNG	Q4trt5	tetraodon n	1395	167.5	5.3	777	2	Q282P9_DROPS	Q282p9 drosophila
1323	169.5	5.4	760	2	Q9TOK5_ARATH	Q9tok5	arabidopsis	1396	167.5	5.3	794	2	Q6YW99_ORYSA	Q6yw99 oryza sativ
1324	169.5	5.4	876	2	Q67WB5_ORYSA	Q67wb5	oryza sativ	1397	167.5	5.3	838	1	TLR4_CRIGR	Q9wv82 cricetus
1325	169.5	5.4	991	1	FLRI3_MOUSE	Q6r5n8	mus musculus	1398	167.5	5.3	886	2	Q469S7_METBF	Q469s7 methanosarc
1326	169.5	5.4	1271	1	TLRI1_MOUSE	Q9jj28	mus musculus	1399	167.5	5.3	939	2	Q4SZU0_TETNG	Q4szu0 tetraodon n
1327	169.5	5.4	1545	2	Q29P78_DROPS	Q29p78	drosophila	1400	167.5	5.3	1112	2	Q4G2W2_LYCPM	Q4g2w2 lycopersico
1328	169	5.4	168	2	Q2VGG9_PETWA	Q2vvg9	petromyzon	1401	167.5	5.3	1112	2	Q41397_LYCPM	Q41397 lycopersico
1329	169	5.4	217	2	Q66WJ6_FELCA	Q66wj6	felis silve	1402	167.5	5.3	1112	2	Q41398_LYCPM	Q41398 lycopersico
1330	169	5.4	273	2	Q5XPK2_ICTPU	Q5xpy6	ictalurus p	1403	167.5	5.3	1263	2	Q5QD1_TETNG	Q5qd1 tetraodon n
1331	169	5.4	279	2	Q58HK2_TRASC	Q58hk2	trachemys s	1404	167.5	5.3	1843	2	Q5QNQ9_MOUSE	Q5qnq9 mus musculus
1332	169	5.4	354	1	PGS2_MOUSE	P28654	mus musculus	1405	166.5	5.3	163	2	Q6E4D4_PETWA	Q6e4d4 petromyzon
1333	169	5.4	354	2	Q3UKR1_MOUSE	Q3ukr1	m 14 days p	1406	166.5	5.3	185	2	Q2VGJ9_PETWA	Q2vgj9 petromyzon
1334	169	5.4	360	2	Q6J0V6_PAROL	Q6j0v6	paralichthy	1407	166.5	5.3	351	2	Q3KQ16_XENLA	Q3kq16 xenopus lae
1335	169	5.4	757	2	Q69MS7_ORYSA	Q69ms7	oryza sativ	1408	166.5	5.3	370	2	Q3ZBN5_BOVIN	Q3zbn5 bos taurus
1336	169	5.4	839	2	Q9RXS7_DEIRA	Q9rxs7	deinococcus	1409	166.5	5.3	483	2	Q5NE36_LISMO	Q5ne36 listeria mo
1337	169	5.4	1175	2	Q4RER3_TETNG	Q4rer3	tetraodon n	1410	166.5	5.3	549	2	Q9SVW8_ARATH	Q9svw8 arabidopsis
1338	169	5.4	1288	2	Q624K5_CAEBR	Q624k5	caenorhabdi	1411	166.5	5.3	582	2	Q5R423_PONPY	Q5r423 pongo pygma
1339	169	5.4	1658	2	Q4PLE9_GIBIN	Q4ple9	gibberella	1412	166.5	5.3	601	2	Q16P98_AEDAE	Q16p98 aedes aegypt
1340	168.5	5.4	169	2	Q2VH97_PETWA	Q2vh97	petromyzon	1413	166.5	5.3	739	2	Q84CF6_LISMO	Q84cf6 listeria mo
1341	168.5	5.4	184	2	Q2VGY2_PETWA	Q2vgy2	petromyzon	1414	166.5	5.3	741	2	Q8KTF0_LISMO	Q8ktf0 listeria mo
1342	168.5	5.4	185	2	Q2VGS5_PETWA	Q2vgs5	petromyzon	1415	166.5	5.3	741	2	Q8KTF9_LISMO	Q8ktf9 listeria mo
1343	168.5	5.4	246	2	Q4KP10_LAMAP	Q4kp10	lampetra ap	1416	166.5	5.3	743	2	Q9SRV9_DRONE	Q9sr9 drosophila
1344	168.5	5.4	255	2	Q66WJ3_FELCA	Q66wj3	felis silve	1417	166.5	5.3	743	2	Q8KTF2_LISMO	Q8ktf2 listeria mo
1345	168.5	5.4	333	2	Q4SWJ28_TETNG	Q4swj28	tetraodon n	1418	166.5	5.3	744	2	Q8KTF1_LISMO	Q8ktf1 listeria mo

1419	166.5	5.3	744	2	Q8KTF5_LISMO	Q8ktf5	listeria	mo	1492	164.5	5.2	805	2	Q658W7_HUMAN	Q658w7	homo sapien
1420	166.5	5.3	744	2	Q8KTF8_LISMO	Q8ktf8	listeria	mo	1493	164.5	5.2	810	2	Q2RBL3_ORYSA	Q2rbl3	oryza sativ
1421	166.5	5.3	744	2	Q8KHNI_LISMO	Q8khni	listeria	mo	1494	164.5	5.2	819	2	Q659A9_HUMAN	Q659a9	homo sapien
1422	166.5	5.3	744	2	Q8KTF8_LISMO	Q8ktf8	listeria	mo	1495	164.5	5.2	858	1	LRC8D_HUMAN	Q7llw4	homo sapien
1423	166.5	5.3	746	2	Q8KTF3_LISMO	Q8ktf3	listeria	mo	1496	164.5	5.2	958	2	Q2RBL3_ORYSA	Q2rbl3	oryza sativ
1424	166.5	5.3	792	2	Q5NE37_LISMO	Q5ne37	listeria	mo	1497	164.5	5.2	1421	2	Q2XXU4_DROPS	Q2xxu4	drosophila
1425	166.5	5.3	794	2	Q2L8H1_LISMO	Q2l8h1	listeria	mo	1498	164.5	5.2	1426	2	Q2XXU5_DROPS	Q2xxu5	drosophila
1426	166.5	5.3	794	2	Q2L8G9_LISMO	Q2l8g9	listeria	mo	1499	164.5	5.2	257	1	LRC3_MOUSE	P59034	mus musculus
1427	166.5	5.3	794	2	Q2L8H2_LISMO	Q2l8h2	listeria	mo	1500	164.5	5.2	257	2	Q543Z4_MOUSE	Q543z4	mus musculus
1428	166.5	5.3	794	2	Q2L8H5_LISMO	Q2l8h5	listeria	mo								
1429	166.5	5.3	794	2	Q2L8H7_LISMO	Q2l8h7	listeria	mo								
1430	166.5	5.3	794	2	Q2L8H4_LISMO	Q2l8h4	listeria	mo								
1431	166.5	5.3	794	2	Q2L8H3_LISMO	Q2l8h3	listeria	mo								
1432	166.5	5.3	797	2	Q4E383_LISMO	Q4e383	listeria	mo								
1433	166.5	5.3	800	1	INLA_LISMF	Q723k6	listeria	mo								
1434	166.5	5.3	800	1	INLA_LISMF	P25146	listeria	mo								
1435	166.5	5.3	800	2	Q45GD5_LISMO	Q45gd5	listeria	mo								
1436	166.5	5.3	800	2	Q45GD6_LISMO	Q45gd6	listeria	mo								
1437	166.5	5.3	1012	2	Q95Y16_ASTPE	Q95y16	asterina	pe								
1438	166.5	5.3	1115	2	Q652D9_ORYSA	Q652d9	oryza	sativ								
1439	166.5	5.3	1215	2	Q60PY2_CABER	Q60py2	caenorhabditis									
1440	166.5	5.3	1270	2	Q7QHP7_ANOQA	Q7qhp7	anopheles	g								
1441	166.5	5.3	1280	2	Q95Y17_ASTPE	Q95y17	asterina	pe								
1442	166.5	5.3	3204	2	Q6X248_ALPH	Q6x248	bovine	hep								
1443	166.5	5.3	163	2	Q6E4F8_PETMA	Q6e4f8	petromyzon									
1444	166.5	5.3	170	2	Q2VKG9_PETMA	Q2vkg9	petromyzon									
1445	166.5	5.3	192	2	Q2VKG1_PETMA	Q2vkg1	petromyzon									
1446	166.5	5.3	245	2	Q4KP01_LAMAP	Q4kp01	lampetra	ap								
1447	166.5	5.3	393	2	Q3UTG8_MOUSE	Q3utg8	mus musculus									
1448	166.5	5.3	426	2	Q72TC3_LEPIC	Q72tc3	leptospira									
1449	166.5	5.3	768	2	Q4SSE3_TETNG	Q4sse3	tetradon	n								
1450	166.5	5.3	806	2	Q6P690_RAT	Q6p690	rattus	norv								
1451	166.5	5.3	835	1	TLR4_RAT	Q9qk05	rattus	norv								
1452	166.5	5.3	971	1	TLR4_RAT	Q2a132	salmo	salar								
1453	166.5	5.3	1030	1	TLR9_PIG	Q5i2m3	sus	scrofa								
1454	166.5	5.3	1030	2	Q8G5R8_PIG	Q8g5r8	sus	scrofa								
1455	166.5	5.3	1110	2	Q7Q768_ORYSA	Q7q768	oryza	sativ								
1456	166.5	5.3	1221	2	Q9N523_CABEL	Q9n523	caenorhabditis									
1457	166.5	5.3	2139	2	Q4PDW0_USTMA	Q4pdw0	ustilago	ma								
1458	165.5	5.3	161	2	Q2VKG0_PETMA	Q2vkg0	petromyzon									
1459	165.5	5.3	169	2	Q2VHG0_PETMA	Q2vhg0	petromyzon									
1460	165.5	5.3	195	2	Q2VGU2_PETMA	Q2vgu2	petromyzon									
1461	165.5	5.3	327	1	Q5RHE5_ERARE	Q5rhe5	brachydanio									
1462	165.5	5.3	360	1	PGS2_BOVIN	P21793	bos taurus									
1463	165.5	5.3	360	1	PGS2_CANFA	Q29393	canis	famil								
1464	165.5	5.3	360	2	Q3MHN1_BOVIN	Q3mhn1	bos taurus									
1465	165.5	5.3	385	2	Q17EE7_AEDA	Q17ee7	aedes	aegypt								
1466	165.5	5.3	526	2	Q7XJ83_ARATH	Q7xj83	arabidopsis									
1467	165.5	5.3	641	2	Q5H716_FUGRU	Q5h716	fugu	rubrip								
1468	165.5	5.3	1005	2	Q3L273_SPAU	Q3l273	sparus	aura								
1469	165.5	5.3	1063	2	Q3L274_SPAU	Q3l274	sparus	aura								
1470	165.5	5.3	1101	2	Q5H957_HUMAN	Q5h957	homo sapien									
1471	165.5	5.3	1256	1	FLII_DROME	Q24020	drosophila									
1472	165.5	5.3	1269	1	FLII_HUMAN	Q13045	homo sapien									
1473	165.5	5.3	1269	1	Q5R4G9_PONPY	Q5r4g9	pongo	pygma								
1474	165.5	5.3	196	2	Q2VH02_PETMA	Q2vh02	petromyzon									
1475	165.5	5.3	283	2	Q4RX02_TETNG	Q4rx02	tetradon	n								
1476	165.5	5.3	436	2	Q5R6F8_PONPY	Q5r6f8	pongo	pygma								
1477	165.5	5.3	780	2	Q299R7_DROPS	Q299r7	drosophila									
1478	165.5	5.3	902	2	Q7R1P2_NEUCR	Q7r1p2	neurospora									
1479	165.5	5.3	955	2	Q32NJ0_XENLA	Q32nj0	xenopus	lae								
1480	165.5	5.3	994	2	Q9C637_ARATH	Q9c637	arabidopsis									
1481	165.5	5.3	1135	2	Q7X812_ORYSA	Q7x812	oryza	sativ								
1482	165.5	5.3	1154	2	Q7QHH4_ANOQA	Q7qhh4	anopheles	g								
1483	164.5	5.2	171	2	Q2VH95_PETMA	Q2vh95	petromyzon									
1484	164.5	5.2	185	2	Q2VGU7_PETMA	Q2vgu7	petromyzon									
1485	164.5	5.2	235	2	Q4GH19_EPTST	Q4gh19	eptretus									
1486	164.5	5.2	437	2	Q1BQ30_9BURK	Q1bq30	burkholderia									
1487	164.5	5.2	468	2	Q4LVE2_9BURK	Q4lve2	burkholderia									
1488	164.5	5.2	582	1	SHOC2_HUMAN	Q9uq13	homo sapien									
1489	164.5	5.2	582	2	Q5VZ63_HUMAN	Q5vz63	homo sapien									
1490	164.5	5.2	582	2	Q5RAV5_PONPY	Q5rav5	pongo	pygma								
1491	164.5	5.2	734	2	Q5R7N1_PONPY	Q5r7n1	pongo	pygma								

ALIGNMENTS

RESULT 1

ID	VASN	HUMAN	STANDARD;	PRT;	673	AA.
AC	Q6EMK4	Q6UML4	Q6UML5	Q96CX1		
DT	18-APR-2006	integrated into UniProtKB/Swiss-Prot.				
DT	16-AUG-2006	sequence version 1.				
DT	25-JUL-2006	entry version 17.				
DE	Vasorin precursor (Protein Slit-like 2).					
GN	Name=VASN; Synonyms=SLITL2; ORFNames=UNQ314/PRO357/PRO1282;					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;					
OC	Catarrhini; Homiidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, INTERACTION WITH TGFB1; TGFB2					
RP	AND TGFB3, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND					
RP	GLYCOSYLATION.					
RX	PubMed=15247411; DOI=10.1073/pnas.0404117101;					
RX	Ikedo Y., Imai Y., Kumeagai H., Nosaoka T., Morikawa Y., Hiseoka T.,					
RA	Nagai R., Kitamura K., Nakaoka T., Imamura T., Miyazono K., Komuro I.,					
RA	"Vasorin, a transforming growth factor beta-binding protein expressed					
RT	in vascular smooth muscle cells, modulates the arterial response to					
RT	injury in vivo."					
RL	Proc. Natl. Acad. Sci. U.S.A. 101:10732-10737(2004).					
RN	[2]					
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT ALA-384.					
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;					
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,					
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,					
RA	Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,					
RA	Huang A., Kim H.S., Klinkowski L., Jin Y., Johnson S., Lee J.,					
RA	Leung L., Liao D., Mark M.R., Robbie B., Sanchez C., Schoenfeld J.,					
RA	Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,					
RA	Vandlen R.L., Watanabe C., Wiedand D., Woods K., Xie M.-H.,					
RA	Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,					
RT	"The secreted protein pJCV, Gray A.M.;"					
RT	effort to identify novel human secreted and transmembrane proteins: a					
RT	bioinformatics assessment."					
RL	Genome Res. 13:2265-2270(2003).					
RN	[3]					
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT ALA-384.					
RC	TISSUE=lung, and Placenta;					
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;					
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,					
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,					
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,					
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,					
RA	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,					
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,					
RA	Brownstein M.J., Ussdin F.B., Itoh Y., Itoh Y., Carninci P., Prange C.,					
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,					
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,					
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,					
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,					
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,					
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,					

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4].
RP GLYCOSYLATION [LARGE SCALE ANALYSIS] AT ASN-117 AND ASN-273, AND MASS
RP SPECTROMETRY.
RX PubMed=16335952; DOI=10.1021/pr0502065;
RA Liu T., Qian W.-J., Gritsenko M.A., Camp D.G. II, Monroe M.E.,
RA Moore R.J., Smith R.D.;
RT "Human plasma N-glycoproteome analysis by immunoaffinity subtraction,
RT hydrazide chemistry, and mass spectrometry.";
RL J. Proteome Res. 4:2070-2080(2005).
CC -1- FUNCTION: May act as an inhibitor of TGF-beta signaling.
CC -1- SUBUNIT: Interacts with TGFBI, TGFBI2 and TGFBI3.
CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein (Probable). Secreted protein.
CC -1- TISSUE SPECIFICITY: Expressed at highest levels in aorta, at
CC intermediate levels in kidney and placenta and at lowest levels in
CC brain, heart, liver, lung and skeletal muscle. Within the aorta,
CC the strongest expression is found in the tunica media of the
CC proximal ascending aorta, the descending thoracic aorta, the
CC abdominal aorta and the coronary arteries. Within the kidney,
CC expression is found in the interstitial cells.
CC -1- PTM: N-glycosylated.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Contains 1 fibronectin type-III domain.
CC -1- SIMILARITY: Contains 11 LRR (leucine-rich) repeats.
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC
CC ENBL; AV166584; AA027704.1; -; mRNA.
CC ENBL; AV358298; AA088665.1; -; mRNA.
CC ENBL; AV358299; AA088666.1; -; mRNA.
CC ENBL; BC013767; AAH13767.1; -; mRNA.
CC ENBL; BC068575; AAH68575.1; -; mRNA.
CC UniGene; Hs.372579; -.
CC HSP; O9BZR6; 1P8T.
CC Ensembl; ENSG00000168140; Homo sapiens.
CC HGNC; HGNC:18517; VASN.
CC MIM; 608843; Gene.
CC RZPD-ProteExp; IOH40553; -.
CC InterPro; IPR006210; EGF.
CC InterPro; IPR000742; EGF_3.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR013032; EGF-like_reg.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR001611; LRR.
CC InterPro; IPR000483; LRR_C.
CC InterPro; IPR000372; LRR_Cys_N.
CC InterPro; IPR003591; LRR_Typ.
CC Pfam; PF00008; EGF_1.
CC Pfam; PF00041; fn3_1.
CC Pfam; PF00560; LRR_1; 8.
CC Pfam; PF01463; LRRCT_1.
CC Pfam; PF01462; LRRNT_1.
CC PRINTS; PR00019; LEURICHRPT.
CC SMART; SM00181; EGF_1.
CC SMART; SM00369; LRR_Typ; 2.
CC SMART; SM00082; LRRCT_1.
CC SMART; SM00013; LRRNT_1.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF_2; 1.
CC PROSITE; PS00026; EGF_3; 1.
CC PROSITE; PS00853; FN3; 1.
CC EGF-like domain; Glycoprotein; Leucine-rich repeat; Membrane;
KW Polymorphism; Repeat; Signal; Transmembrane.
FT SIGNAL 1 23 Potential.

FT	CHAIN	24	673	Vasorin.
FT	TOPO_DOM	24	575	/FTIG=PRO 0000232630.
FT	TRANSMEM	576	586	Extracellular (Potential).
FT	TOPO_DOM	597	673	Potential.
FT	REPEAT	51	74	Cytoplasmic (Potential).
FT	REPEAT	75	98	LRR 1.
FT	REPEAT	100	122	LRR 2.
FT	REPEAT	123	146	LRR 3.
FT	REPEAT	148	168	LRR 4.
FT	REPEAT	169	191	LRR 5.
FT	REPEAT	193	214	LRR 6.
FT	REPEAT	215	240	LRR 7.
FT	REPEAT	241	263	LRR 8.
FT	REPEAT	264	289	LRR 9.
FT	REPEAT	290	310	LRR 10.
FT	DOMAIN	405	442	LRR 11.
FT	DOMAIN	458	555	EGF-like.
FT	CARBOHYD	101	101	Fibronectin type-III.
FT	CARBOHYD	117	117	N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	273	273	N-linked (GlcNAc...)
FT	CARBOHYD	500	500	N-linked (GlcNAc...)
FT	CARBOHYD	528	528	N-linked (GlcNAc...) (Potential).
FT	DISULFID	409	420	N-linked (GlcNAc...) (Potential).
FT	DISULFID	414	430	By similarity.
FT	DISULFID	432	441	By similarity.
FT	VARIANT	384	384	E -> A (in dbSNP:3810818).
FT	CONFLICT	70	70	/FTIDEVAR 025991.
FT	CONFLICT	91	165	G -> S (in Ref. 2; AA088665).
FT	SEQUENCE	673	AA; 71713	Missing (in Ref. 2; AA088665).
FT	SEQUENCE	673	AA; 71713	MW; 891E149652DEA286 CRC64;
QY	1	MCSRVP	LLPLLL	LALGPGVQCSPGCGCQSQPQTVECTARQGTTPVDRVPPDTVGLYVF 60
DB	1	MCSRVP	LLPLLL	LALGPGVQCSPGCGCQSQPQTVECTARQGTTPVDRVPPDTVGLYVF 60
QY	61	ENGITM	DASSFAGLPGLQLDLSQNIAS	----- 90
DB	61	ENGITM	DASSFAGLPGLQLDLSQNIAS	----- 120
QY	91	-----	-----	-----LRLPRLLLDLSHNS 105
DB	121	RLRLRL	LYLGNRIH	OPGAFDTLRLLELKLQDNEURLPRLPRLPRLLLDLSHNS 180
QY	106	LLALEP	GILDTANVEALRLAGLQQLDEGLFSRLNHLHDVSDNQLERVPVIRGLRG 165	
DB	181	LLALEP	GILDTANVEALRLAGLQQLDEGLFSRLNHLHDVSDNQLERVPVIRGLRG 240	
QY	166	LTRLR	LAGNTRIAQLRPEDLAGLAQLDVSNSLQALPGDLSGLFPRLRLAAARNPF 225	
DB	241	LTRLR	LAGNTRIAQLRPEDLAGLAQLDVSNSLQALPGDLSGLFPRLRLAAARNPF 300	
QY	226	NCVCP	LSWFGPWRVRESHVTLASPEETRCCHFPKKNAGRLLELDYADFGCPATTTATVPT 285	
DB	301	NCVCP	LSWFGPWRVRESHVTLASPEETRCCHFPKKNAGRLLELDYADFGCPATTTATVPT 360	
QY	286	TRPVV	REPTALSSSLAPTWSLPTAPATEAPSPSTAPPTVGPVPQDCPSTCLNGGTC 345	
DB	361	TRPVV	REPTALSSSLAPTWSLPTAPATEAPSPSTAPPTVGPVPQDCPSTCLNGGTC 420	
QY	346	HLGTR	HHLACLCEPGTGLYCYSQMGQTRPSTPTVTPRPRSLTGLIEVPSVLSVGL 405	
DB	421	HLGTR	HHLACLCEPGTGLYCYSQMGQTRPSTPTVTPRPRSLTGLIEVPSVLSVGL 480	
QY	406	QRYLC	SSVQLRSRLTYRNLSGPKRLVTLRLPASLAETVTLQRENATYSVCVMPPLGP 465	
DB	481	QRYLC	SSVQLRSRLTYRNLSGPKRLVTLRLPASLAETVTLQRENATYSVCVMPPLGP 540	
QY	466	GRVPE	GEACGEAHTPPAVHSNHAPVTQAREGNLPLLLIAPALAAVLLAALAAVGAAYCVR 525	

Query Match 98.2%; Score 3078.5; DB 1; Length 673;
Best Local Similarity 88.6%; Pred. No. 1.8e-166; Indels 75; Gaps 1;
Matches 596; Conservative 0; Mismatches 2;

Db 541 GRVPEGEACGEATTPPAVNSHNPVTQAREGNPLLLIAPALAAVLAAAVGAACVCR 600
 QY 526 RGRAMAAADKQGVGAGGLEGVKVPLEPGPKATGGGALPGSSCEVPLMGFP 585
 Db 601 RGRAMAAADKQGVGAGGLEGVKVPLEPGPKATGGGALPGSSCEVPLMGFP 660
 QY 586 PGLQSPHAKPYI 598
 Db 661 PGLQSPHAKPYI 673

RESULT 2
 VASN_MOUSE
 ID VASN_MOUSE STANDARD; PRT; 673 AA.
 AC Q9CZT5; Q8BJJ0; Q8R2G5;
 DT 18-APR-2006, integrated into UniProtKB/Swiss-Prot.
 DT 18-APR-2006, sequence version 2;
 DT 13-JUN-2006, entry version 29;
 DE Vasorin precursor (protein Slit-like 2).
 GN Name=Vasrn; Synonym=Slit12;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC STRAIN=C57BL/6J;
 RA Schrewe H., Kutejova E.;
 RT "Structure and expression analysis of the mouse Slit-like 2 (Slit12) gene";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 [2]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP STRAIN=C57BL/6J;
 RC PubMed=16141072; DOI=10.1126/science.1112014;
 RX Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Bansal K.P., Baxter L., Belsel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G., Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E., Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Humintek L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakaguchi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G., Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schoenbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka E., Sugiyara K., Sultana R., Takenaka Y., Taki K., Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Imamura K., Itoh T., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,

RA Hayaishizaki Y.;
 RT "The transcriptional landscape of the mammalian genome";
 RL Science 309:1559-1563 (2005).
 [3]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP STRAIN=FVB/N; TISSUE=Kidney;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [4]
 RN DEVELOPMENTAL STAGE, AND INDUCTION.
 RP PubMed=15247411; DOI=10.1073/pnas.0404117101;
 RX Ikeda Y., Inai Y., Kumagai H., Nosaka T., Morikawa Y., Hisaka T., Maeda I., Maemura K., Nakaoka T., Imamura T., Miyazono K., Komuro I., Nagai R., Kitamura T.;
 RT "Vasorin, a transforming growth factor beta-binding protein expressed in vascular smooth muscle cells, modulates the arterial response to injury in vivo";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:10732-10737 (2004).
 CC -1- FUNCTION: May act as an inhibitor of TGF-beta signaling (By similarity).
 CC -1- SUBUNIT: Interacts with TGFBI, TGFBI2 and TGFBI3 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane protein (Probable).
 CC -1- DEVELOPMENTAL STAGE: Expression begins at E10.5 and increases as development progresses to E17.5. Expression rises in parallel with the differentiation of vascular smooth muscle cells (VSMCs) of the aorta.
 CC -1- INDUCTION: Upon retinoic acid-induced differentiation of smooth muscle cells in vitro.
 CC -1- PTM: N-glycosylated (By similarity).
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Contains 1 fibronectin type-III domain.
 CC -1- SIMILARITY: Contains 11 LRR (leucine-rich) repeats.
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 DR ENBL; AJ458938; CAD30331.1; -; mRNA.
 DR ENBL; AK012169; BAB28075.1; -; mRNA.
 DR ENBL; AK083684; BAC38992.1; -; mRNA.
 DR ENBL; AK132325; BAE21105.1; -; mRNA.
 DR ENBL; BC050274; AAH50274.1; -; mRNA.
 DR HSP; Mm.248337; -.
 DR HSP; P00740; LEDM.
 DR Ensembl; ENSMUSG00000039646; Mus musculus.
 DR MGI; MGI:2177651; Vasn.
 DR InterPro; IPR006210; EGF.
 DR InterPro; IPR000742; EGF_3.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR013032; EGF-like_reg.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR016111; LRR.
 DR InterPro; IPR000483; LRR_C.

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DR InterPro: IPR000372; LRR_cys_N.
DR InterPro: IPR003591; LRR_typ.
DR Pfam: PF00008; EGF_1.
DR Pfam: PF00041; fn3_1.
DR Pfam: PF00560; LRR_1; 7.
DR Pfam: PF01463; LRRCT; 1.
DR Pfam: PF01462; LRRNT; 1.
DR PRINTS: PR00019; LEURICHRPT.
DR SMART: SM00181; EGF_1.
DR SMART: SM00600; FN3_1.
DR SMART: SM00369; LRR_TYP; 7.
DR SMART: SM00082; LRRCT; 1.
DR SMART: SM00013; LRRNT; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00026; EGF_3; 1.
DR PROSITE: PS00853; FN3; 1.
KW EGF-like domain; Glycoprotein; Leucine-rich repeat; Membrane; Repeat;
FT SIGNAL 1 24
FT CHAIN 25 673

FT TOPO_DOM 25 576
FT TRANSMEM 577 597
FT TOPO_DOM 598 673
FT REPEAT 52 75
FT REPEAT 76 99
FT REPEAT 101 123
FT REPEAT 124 147
FT REPEAT 149 169
FT REPEAT 170 192
FT REPEAT 194 215
FT REPEAT 216 241
FT REPEAT 242 264
FT REPEAT 265 287
FT REPEAT 289 311
FT DOMAIN 406 443
FT DOMAIN 459 556
FT CARBOHYD 102 102
FT CARBOHYD 118 118
FT CARBOHYD 274 274
FT CARBOHYD 501 501
FT CARBOHYD 529 529
FT CARBOHYD 555 555
FT DISULFID 410 421
FT DISULFID 415 431
FT DISULFID 433 442
FT CONFLICT 225 225
FT CONFLICT 383 383
SQ SEQUENCE 673 AA; 72261 MW; AAB8DA82DA8E9D32 CRC64;

Query Match 79.4%; Score 2490; DB 1; Length 673;
Best Local Similarity 73.5%; Pred. No. 4.6e-133;
Matches 491; Conservative 25; Mismatches 74; Indels 78; Gaps 3;

QY 6 PLLPLLLLLALGSGVGGSGGCGSQSPQTVFCTARQGTTPRDPVPTVGLYFENGIT 65
DB 9 PLL-LLLLLLGSGVGGSGGCGSQSPQTVFCTARQGTTPRDPVPTVGLYFENGIT 66
QY 66 MLDASSFAGLPGLQLLDLSNQNIAS----- 90
DB 67 TLDVGCFAGLPGLQLLDLSNQNIATSLPGGTFQPLVNLNLDLTANKLHEISNETFGLRR 126
QY 91 -----LRLPRLLDLSHNSLALE 110
DB 127 LERLYLGNRIHQPGAFDALDRLLKLPDNLRLVPLPLPRLLDLSHNSIAPALE 186
QY 111 PGILDTANVEALRLAGLQQLDDEGLFSRLNLHDLVDSDNQLERVPVIRGLGLTLRL 170
DB 187 AGILDTANVEALRLAGLQQLDDEGLFSRLNLHDLVDSDNQLHMPSVIQGLRGLTLRL 246
QY 171 LAGNTRIAQLRPEDLAGLALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFCVCP 230
DB 171 LAGNTRIAQLRPEDLAGLALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFCVCP 230
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DB 247 LAGNTRIAQIRBEDLAGLTALQELDVSNLSLQALPSDLSSLFPRLRLAAARNPFCVCP 306
QY 231 LSWFGPWVRESHVTLASPEETRCHFPKPNAGRLLLLDYADFCGPATTTTATVPTTRPVV 290
DB 307 LSWFGPWVRENHVTLASPEETRCHFPKPNAGRLLLLDYADFCGPVTTTATVPTTIRSTI 366
QY 291 REPTLSSSLAPTWSPTAPATEAPSPPTAPPTVGPVQPDQCPSTCLNGTCHLGTTR 350
DB 367 REPTLSSSOAPTWSPTAPATEAPSPPTAPPTVGPVQPDQCPSTCLNGTCHLGTTR 426
QY 351 HHLACLCPGFTGLYCESQMGQTRSPPTVPRPSRLTLGLEPVSPTSRLVGLORYLQ 410
DB 427 HHWECLCPGFTGLYCESQMGQTRSPPTVPRPSRLTLGLEPVSPTSRLVGLORYLQ 486
QY 411 GSSVQLRSLRLTYRNLSGDPKRLVTLRLPASLAETVTLQRPNATYSVCVMPGPGRVPE 470
DB 487 GNTVQLRSLRLTYRNLSGDPKRLVTLRLPASLAETVTLQRPNATYSVCVMPGPGRVPE 546
QY 471 GEEACGEAHTPPAVHSNHAPVTOAREGNLPLLIAPALAAVLLAAVGAAYCVRGRAM 530
DB 547 GEEACGEAHTPPAVHSNHAPVTOAREGNLPLLIAPALAAVLLAAVGAAYCVRGRAM 605
QY 531 AAAAQKQGVGPGAGPLEGKVPLEPGKATEGCGEALPSGCECEVPLMGEPGCLQS 590
DB 606 TSTAQDKGVGPGTGLGKVPLEPGKATEGCGEALPSGCECEVPLMGEPGCLQS 665
QY 591 PLHAKPYI 598
DB 666 VLPKHYI 673

RESULT 3
VASN_XENTR STANDARD; PRT; 661 AA.
ID VASN_XENTR STANDARD; PRT; 661 AA.
AC Q6DFS5;
DT 18-APR-2006, integrated into UniProtKB/Swiss-Prot.
DT 16-AUG-2004, sequence version 1.
DT 30-MAY-2006, entry version 15.
DE Vasorin precursor.
GN Names: vasn;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
OX NCBI_TaxID=8364;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RG NIH - Xenopus Gene Collection (XGC) project;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May act as an inhibitor of TGF-beta signaling (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein (Probable).
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 fibronectin type-III domain.
CC -!- SIMILARITY: Contains 11 LRR (leucine-rich) repeats.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonCommercial-ShareAlike license
CC
CC EMBL: BC076988; AAH76988.1; -; mRNA.
DR UniGene: Str. 8462;
DR InterPro: IPR008985; ConA_like_lec_gl.
DR InterPro: IPR006210; EGF.
DR InterPro: IPR000742; EGF_3.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR013032; EGF_like_reg.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_C.
DR InterPro: IPR003591; LRR_typ.
DR Pfam: PF00008; EGF_1.
DR Pfam: PF00560; LRR_1; 8.
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Db 6 PLSHLILQLLCCGLSSRCHDCTCLPSNNIFCQVRLNLYMPRLPGTGRQLYVFQNKIN 65
Qy 66 MLDASSFAGPGQLQLDLSONQA-----89
Db 66 ILQODDFVELGEMLDLSQNSUSEIPDGVPFSLSSLHNLDSNYTHISKDSFTGLVN 125
Qy 90 -----SIRLPRLLLLDLSHNSLLALE 110
Db 126 LERLYLSNIQIHPAAFEGLNLELKLQGNQISVLPAQLPRLLHLDLSYNSIPPLV 165
Qy 111 PGILDTANVALRAGLGLQOLDEGLFSLRLNHLHDLDVSNQLERVPPVIRGLRGLTRLR 170
Db 186 AQDLQTPHLESKIAGLGLSLDBELLSGLVNLHVLVDVSNQVLDIQTLSKMGGLRLN 245
Qy 171 LAGNTRIAQLRPEDLAGLAALQELDVSNLSIQALPGDLSGLFPRLLRLLAARPNPCVCP 230
Db 246 LTGNP-LGSLKHEDFQNLVNLLELDLSNLQGFPGFFNLFPLKLEKLTAAENPNCCLP 304
Qy 231 LSWFGPVRVRESHVTLASPESTRCHFPFPKNAGRLLELDYADFGCPATTTTATVTPRPVV 290
Db 305 LANFPALWKDVRVLLRTSTRCHFPFPINSKVLKLEHKGFCPTTIELTSAGTSSTT 364
Qy 291 REPTALSSSLAPTWLSTAPATAPSPSTAPTPVGPVQP-----QD-----CP 335
Db 365 SKPKNSSTQLGTHIVPPAP-----PSDISSADADNFPVYQTTAFPPSRIMEDSEGEIMCP 420
Qy 336 PSTCLNGTCHLGRHLHCLCPGFTGLYCSEMGQGTPTPTP-----VTPRPPRS 368
Db 421 PNICLNGTCTFKNSEGVIVCLCPSPMSGNYCEIQ-NEAMLPSPSRVSLTIATVQBN-- 477
Qy 389 LTLGIEVSPSTSLRVGLQRYLQSSVQLSLRLTYRLNLSPDKRLVTLRLPASLAETVT 448
Db 478 -TSSHHITSTSLDLHRYQ-TRPHIRGLTYSLNSLQDPRPLQSLVPPSPVEYTLR 535
Qy 449 QLRPNATYSYCVNPLGPRVPEGEAECAHT---PPAVHSHNAPVTQAREGNLPLLIAP 505
Db 536 GLOPNSTYSVCASPLGE-PVHASVSACWEARTAGIPSSSHEPSVDRTEPSSSLTPVW-- 592
Qy 506 ALAAVLLAALAAVGAACVVRGRAMAAADKQGVGAGPGLGKVPLEBG---PK 561
Db 593 AVAVVMVVAIAT-VVVISRRRRKAPVMDLHE---TSPLEMEGVKTNPENGLTHPK 646
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RESULT 5

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Q503G2 BRARE PRELIMINARY; PRT; 643 AA.
AC Q503G2;
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-JUN-2005, sequence version 1.
DT 13-JUN-2006, entry version 10.
DE Slit-like 2.
GN Name=vaen;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Singapore local strain; TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uadin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Boeak S.A., McWain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Qy 29.6%; Score 927.5; DB 2; Length 643;
Best Local Similarity 36.4%; Pred.No. 2.2e-44;
Matches 224; Conservative 77; Mismatches 201; Indels 113; Gaps 14;
Qy 46 VPRDVPDPVTGLYVFENGITMLDASSFAGLPGQLDLSONQA-----89
Db 1 MPRGLPSTGKLYVFQNKINILQOQDFVELGEMLDLSQNSLSBIPDGVPFSLSSLHNL 60
Qy 90 -----S 90
Db 61 DLSSNITHSKDSFTGLVNLRLYLSNIQIHPAAFEGLNLELKLQGNQISVLPA 120
Qy 91 LRLPRLLLDLSHNSLLALEPGILDTANVALRAGLGLQOLDEGLFSLRLNHLHDLDVSD 150
Db 121 LQLPRLLHLDLSYNSIPPLVAQDLQTPHLESKIAGLGLSLDBELLSGLVNLHVLVDV 180
Qy 151 NQLERVPPVIRGLRGLTRLRKLQNTRIAQLRPEDLAGLAALQELDVSNLSIQALPGDLSG 210
Db 181 NQLVDIQTPLSKMGGLRLNLTGNP-LGSLKHEDFQNLVNLLELDLSNLQGFPGFFN 239
Qy 211 LFLRLRLAARPNPCVCPSLSWFGPVRVRESHVTLASPESTRCHFPFPKNAGRLLELDYA 270
Db 240 LFLPKLEKLTAAENPNCCLCPAWPDLKDVVRVLLRTSTRCHFPFPINSKVLKLEH 299
Qy 271 DFGCPATTTTATVTPRPVREPTALSSSLAPTWLSTAPATAPSPSTAPTPVGPVQP 326
Db 300 DFGCPITTIETLSAGTSSTTSKTSNSTSQSGTTHIVPPALPSDISSADADNFPVYQTAF 359
Qy 327 PVQPQD-----CPSTCLNGTCHLGRHLHCLCPGFTGLYCSEMGQGTPTPTPT 379
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Db 360 PSIMEDSEGEIMCPNCLNGGTCIFKSNVIVCLCPSPMSGLYCEIQ-NEAMLPPPS 418
 QY 380 P-----VTPRPRSLTGLIEVPSVSLRVLQYSSVOLRSRLRLTYRNLSPGDKR 432
 Db 419 PRVSLTETATVQPN--TSSHSITSTISLDLHRVIQ-TRPHIRGIRLTYSLSGPDRR 474
 QY 433 LVTLRPLASLAETVTLRNRNATYSVCVMPGLGPRVPEGEACGEAHT---PPAVHSNHA 489
 Db 475 PLQLSVPPSPPEYTLRGLQPNSTYSVCASPLGE-PVHASVSACMEARTAGIPSSHEPSV 533
 QY 490 PVTQAREGNPLLIAPALAAVLLAALAAVGAAYCVRRRGMAAAADKQGVGPGAGPLEL 549
 Db 534 DRETPSSSLTPVV--AVAVVMVVAIIAT-VVVISRRRRPKAPVMDLHE-----TSPLEM 586
 QY 550 EGKVPLEPG---PK 561
 Db 587 EGKVTNPENGLTHPK 601

RESULT 6

Q4SQ68_TETNG PRELIMINARY; PRT; 962 AA.
 AC Q4SQ68;
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2005, sequence version 1.
 DT 02-MAY-2006, entry version 7.
 DE Chromosome 19 SCFA14535, whole genome shotgun sequence.
 GN ORFNAMES=GSTENG00014497001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15496914; DOI=10.1038/nature03025;
 RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Briemont C., Skalli Z., Cattoilco L., Poulain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope, Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.

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 CC -----
 CC EMBL; CA001014535; CAP97214.1; -; Genomic_DNA.
 CC GO; GO:0005634; C:nucleus; IEA;
 CC GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 CC InterPro; IPR000742; EGF_3.
 CC InterPro; IPR006209; EGF-like.
 CC InterPro; IPR013032; EGF-like_reg.
 CC InterPro; IPR003961; FN_III.
 CC InterPro; IPR008957; FN_III-like.
 CC InterPro; IPR001611; LRR.
 CC InterPro; IPR000483; LRR_C.

RESULT 7

LRC24_HUMAN
 ID LRC24_HUMAN STANDARD; PRT; 513 AA.
 AC Q50LGS;
 DT 04-APR-2006, integrated into UniProtKB/Swiss-Prot.
 DT 07-JUN-2005, sequence version 1.
 DT 30-MAY-2006, entry version 10.
 DE Leucine-rich repeat-containing protein 24 precursor.
 GN Name=LRC24;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
 OC Catarrhini; Hominoidea; Homidae; Homo.
 OX NCBI_TaxID=9606;

DR InterPro; IPR003591; LRR typ.
 DR InterPro; IPR005033; YEATS.
 DR Pfam; PF00008; EGF_1.
 DR Pfam; PF00560; LRR_1; 8.
 DR Pfam; PF03366; YEATS; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00369; LRR_TYP; 2.
 DR SMART; SM00082; LRRCT; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS00853; FN3; 1.
 DR PROSITE; PS1037; YEATS; 1.
 SQ SEQUENCE 962 AA; 106856 MW; 3EC2C9402AC80BF6 CRC64;

Query Match 29.2%; Score 914.5; DB 2; Length 962;

Best Local Similarity 38.0%; Pred. No. 1.8e-43;

Matches 222; Conservative 77; Mismatches 190; Indels 95; Gaps 18;

QY 57 LVVFENGITMLDASSFAGLPGQLLDLSONOTA---SLRLPRLLLDLHNSLLEPGI 113
 Db 388 LYLHGNLIQSIHAEAFEGLEMLELEKLGQNGUSSLRPPRLLDLHNSLPSGPD 447
 QY 114 LDTANVEALRLAGLGLQQLDEGLFSLRLNLDHLDVSDNQLERVPVIR--GLRGLRLRL 171
 Db 448 FQTPHLEALKIVSLGLMSLGDLELIASMRNLHLDISMNQLTEVPLALKQDSLKGLKLSL 507
 QY 172 AGNTRIAQLRPEDLAGLAALQELDVNSLSQALPGDLSGLFPRLRLAAARNPFCVCP 231
 Db 508 AGNP-LGDLRVEDFEKLTSLQELDLGLNQLQSPSPFLFMFRLTQLTAAENPNCICPL 566
 QY 232 SWFGPVRVSHVTLASPESTRCHFPKPNAGRLLELDYADFGCPATTATVTPVVR 291
 Db 567 AMFPVWLKCKVNLRRPPESTRCHFPKPNAGRLLELDYADFGCPATTATVTPVVR 618
 QY 292 EPTALSSSLAPTWSLTAPATEAPSPSTAP-----PTVGPVPQPOD----- 333
 Db 619 SPTGTSFSPVSTTPPKMTYTNAPPPPPSEIILPKTYPPLPEPTSPSTSGEVE 678
 QY 334 ---CPSTCLNGTCHLGRHHLACLCPGFTGLYCESQMGQCTRPSPVTPRPR--- 387
 Db 679 SHICPANI CLNGTCHFDPMGQLSCICLSTGLYCEN-----VDIVDPKHPV 728
 QY 388 ---SLTLGIEP-----VSPTSRLVQLQYSSVOLRSRLTYRNLSPGDKRLV 434
 Db 729 TEATLAASSVPVQNDIAISSRQVTSITLILDLQRFIE-TRPHIRGIRLIYRNLSPDRPM 787
 QY 435 TLRLPASLAETVTLRPNATYSVCVMPGLP-----GRVPEGEACGEAHT----- 480
 Db 788 ILSPASYPETLRLGKPNCTYSVCASPLGERVSLRANSSVDTG--SCTEARTEGILMTS 845
 QY 481 PPAVHSNHAPVTOAREGNPLLIAPALAAVLLAALAAVGAAYCVRRRGMAAAADKQGV 540
 Db 846 SSATAPTGPMT-----FTLILAVSALALVLGSLVAGTVICVRK-RREAKAGMELEMA 898
 QY 541 GPGAGPLEGVKVPLEPGPKATEGGEALPSG-----SCEVPL 580
 Db 899 PADSDPMELDKMLGLEANGT-----LPHKQAQINRCHTFL 936

RA NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Brain;
RA Shimizu N., Asakawa S., Shimizu A., Yamazaki S., Ishikawa S.K.;
RT "Novel gene containing leucine rich repeat on human chromosome 8.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
[2]
RA NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Haie S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Membrane; single-pass membrane protein
(Potential).
CC -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
domain.
CC -!- SIMILARITY: Contains 7 LRR (leucine-rich) repeats.
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DR EMBL: AB178281; BAD97811.1; -; mRNA.
DR EMBL: BC110677; AA110681.1; -; mRNA.
DR UniGene: Hs.591399; -.
DR HGNC: HGNC:28947; LRR24.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR013098; Ig-sub.
DR InterPro: IPR003599; Ig-sub.
DR InterPro: IPR003598; Ig-sub2.
DR InterPro: IPR016111; LRR.
DR InterPro: IPR000483; LRR_C.
DR InterPro: IPR00372; LRR_Cys_N.
DR InterPro: IPR003591; LRR_Cys.
DR Pfam: PF07679; I-set; 1.
DR Pfam: PF00560; LRR_1; 5.
DR Pfam: PF01463; LRRCT; 1.
DR PRINTS: PR00019; LEURICHRPT.
DR SMART: SM00409; IG; 1.
DR SMART: SM00408; IGC2; 1.
DR SMART: SM00369; LRR_TYP; 3.
DR SMART: SM00082; LRRCT; 1.
DR SMART: SM00013; LRRNT; 1.
DR PROSITE: PS00835; IG LIKE; 1.
KW Glycoprotein; Immunoglobulin domain; Leucine-rich repeat; Membrane;
Repeat; Signal; Transmembrane.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 513 Leucine-rich repeat-containing protein
/FTID=PRO_0000231596.
FT TRANSMEM 406 Potential-
FT REPEAT 49 72 LRR 1.
FT REPEAT 73 96 LRR 2.
FT REPEAT 98 120 LRR 3.
FT REPEAT 122 144 LRR 4.

FT REPEAT 145 168 LRR 5.
FT REPEAT 170 192 LRR 6.
FT REPEAT 244 265 LRR 7.
FT DOMAIN 260 361 Ig-like C2-type.
FT COMPBIAS 375 378 Poly-Pro.
FT COMPBIAS 427 432 Poly-Arg.
FT CARBOHYD 334 334 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 363 363 N-linked (GlcNAc...) (Potential).
FT DISULFID 281 345 By similarity.
SQ SEQUENCE 513 AA; 55199 MW; 3770FA80D979CIDE CRC64;
Query Match 11.8%; Score 368.5; DB 1; Length 513;
Best Local Similarity 26.4%; Pred. No. 9.3e-13;
Matches 170; Conservative 63; Mismatches 217; Indels 195; Gaps 28;
QY 1 MCSRVPLLELLLLALGPGVCGSCGSCSQSQVTFCTARQGTTPVDRVPPDVTGLVVF 60
DB 1 MAURAPALLPULLLL-LPLRAAGCPAACRC-YSATVECGALRLRVPLGIPPGTQLFLQ 58
QY 61 ENGITMIDASSFAGLPGLQLDLDSQNIASRL-----PRLLLDLSHNSLLALBPG-I 113
DB 59 DNNIARLEPCALAPLAALRLYLHNSLRALAEAGAPRAQPRLELALTSNRLRLRSAGAF 118
QY 114 LOTANVEALRLAGLIGLQQLDEGLFSRLNHLHDVSDNQLERVPVIRGLRGLTRRLAG 173
DB 119 VGLAQLRVLYLAGNQLARLLDFTFLPLRLQLHLQENSTIE----- 159
QY 174 NTRIAQLRPEDLAGLAALQELDVNSLSLQALPGDLSGLFPLRLLLAAARNPFNCVCLSW 233
DB 160 -----LLEDAQLAGLSLLDLNRNLQGTISREALQPLASQLVLRITENPWRCDCAHW 214
QY 234 FGPWVRESHVTLASPEETR--CHFPKPNAGRLLELDYADFGPCATTATTTVTPTRVVR 291
DB 215 LGAWKEGGQRLTSRDKIMCAEPRLALQSLLDVSHSLIC-----IPPSVHV-- 264
QY 292 EPTALSSSLAPTWSPTAPATEAPSPPTAPTPVGPVPQDCPP--STCLNGGTCHLGT 349
DB 265 QPLELTANLGED-LRVACQASGYQP-----LVTRWKVPQPREGRPRAQAQLEGGL--LGL 317
QY 350 RHHLACLCPGEGF-----TGLY-CESQMGG-----TRSP-TPVTPRP 385
DB 318 GHSAADTSGGMLFLSNITLAHAGKYECEASNAGGAARVFRLLVNASRQOQPAQPPP 377
QY 386 PRSLTLGIEPVSPSTSLRVGLQRYLOGSSVQLRSLTYRNLSPGDKRLVLRPASLAEY 445
DB 378 PAAPAGSEP----- 387
QY 446 TVTQLRPNATYSVCMPLGPRVPEGEAEACGEAHTPPAVHSHNAPVTOAREGNLPLLIAP 505
DB 388 -----RPEAG-SMAFRALG-----VATQT-----AIAA 409
QY 506 ALAAVLLAALAAVGAAYCVPRGRAMAAQDKQGVPGA-----GP---LEEGVK- 553
DB 410 AIALALTALLLV-AMICRRRRRKKK-----RGPPEGALFVNDYDGPCTFAQLLELRD 464
QY 554 -----VPLEPGFKATGEGEALPGSECEVPLMGPPGPGLOSP 591
DB 465 ERGHEMFVINSKPLFAEGPAEA---PADCG-PAQG-AGPGLRVP 504
RESULT 8
LRFN4_HUMAN
ID LRFN4_HUMAN STANDARD; PRT; 635 AA.
AC Q9PJG9; Q9BNJ0;
DT 29-MAR-2005, integrated into UniProtKB/Swiss-Prot.
DT 05-JUL-2004, sequence version 1.
DT 13-JUN-2006, entry version 27.
DE Leucine-rich repeat and fibronectin type-III domain-containing protein
DE 4 precursor.
GN Name=LRFN4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;

OC Catarrhini; Hominidae; Homo.
 RN NCBI_TaxID=9606;
 RP [1]
 RC TISSUE=Eye, and Lung;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Brange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
 CC protein (Potential).
 CC -!- SIMILARITY: Contains 1 fibronectin type-III domain.
 CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
 CC -!- SIMILARITY: Contains 7 LRR (leucine-rich) repeats.
 CC -----
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 CC -----
 CC
 DR EMBL: BC000207; AAH00207.2; -; mRNA.
 DR EMBL: BC015581; AAH15581.2; -; mRNA.
 DR UniGene: Hs.209979;
 DR Ensembl: ENSG00000173621; Homo sapiens.
 DR HGNC: HGNC:28456; LRFNA.
 DR LinkHub: Q6PJG9;
 DR RZPD-ProtExp: IOH23019; -;
 DR RZPD-ProtExp: V0090; -;
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR013098; Ig I-set.
 DR InterPro: IPR003599; Ig_sub.
 DR InterPro: IPR003598; Ig_sub2.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_C.
 DR InterPro: IPR003591; LRR_type.
 DR Pfam: PF00041; fn3; 1.
 DR Pfam: PF07679; I-set; 1.
 DR Pfam: PF00560; LRR_1; 5.
 DR PRINTS: PR00019; LEURICHRPT.
 DR SMART: SM00060; FN3; 1.
 DR SMART: SM00409; IG; 1.
 DR SMART: SM00408; IGC2; 1.
 DR SMART: SM00369; LRR_TYP; 2.
 DR SMART: SM00082; LRRCT; 1.
 DR PROSITE: PS50853; FN3; 1.
 DR PROSITE: PS50853; IG LIKE; 1.
 DR Glycoprotein; Immunoglobulin domain; Leucine-rich repeat; Membrane;
 KW Polymorphism; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 16 Potential
 FT CHAIN 17 635 Leucine-rich repeat and fibronectin type-III domain-containing protein 4.
 FT FT /FTid=PRO_0000014843.
 FT FT
 FT TOPO_DOM 17 518 Extracellular (Potential).
 FT TRANSMEM 519 539 Potential.
 FT TOPO_DOM 540 635 Cytoplasmic (Potential).
 FT REPEAT 46 70 LRR 1.
 FT REPEAT 71 94 LRR 2.

FT REPEAT 95 118 LRR 3.
 FT REPEAT 120 142 LRR 4.
 FT REPEAT 144 167 LRR 5.
 FT REPEAT 168 191 LRR 6.
 FT REPEAT 193 216 LRR 7.
 FT DOMAIN 201 367 Ig-like.
 FT DOMAIN 368 492 Fibronectin type-III.
 FT CARBOHYD 25 25 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 70 70 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 324 324 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 333 333 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 376 376 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 440 440 N-linked (GlcNAc...) (Potential).
 FT DISULFID 302 351 By similarity.
 FT VARIANT 340 340 V -> A (in dbSNP:3741194).
 FT /FTid=VAR_024499.
 SQ SEQUENCE 635 AA; 66860 MW; 13E66645A17A92EE CRC64;
 Query Match 11.5%; Score 359.5; DB 1; Length 635;
 Best Local Similarity 27.6%; Pred. No. 3.8e-12;
 Matches 169; Conservative 61; Mismatches 281; Indels 101; Gaps 23;
 QY 8 LALPLLLALLGPGVQVCGPCGQC---SQPTVFCTARQGTTPRDPVPPDTVGLYVFENG 64
 DB 1 MAPPLLLLLLGGAAACPLPCVQNLSESLTCAHGLLFVPPVDRRTVELRLADNFI 60
 QY 65 TMLDASSAGLPGQLQLDLSONQIASL-----RLPRLLLDLSHNSLALPEGL-DTA 117
 DB 61 QALGPPDFRMTGLVDTLSRNAITRIGARAFGLDLSRLHLDGNRLVELGTSLRGPV 120
 QY 118 NVEALRLAGLQQLDDEGLFSR-LRNLDHLDVSDNQLERVP-PVIRGLRGLTLRLAGNT 175
 DB 121 NLOHLTLGNQLRITAPGAPDFLESLDLDLSYNNLRQVPWAGIAMPALHTLNLHNL 180
 QY 176 RLQAQLRPEDLAGLAALQELDLSNLQALPGDLSGLFPRLR-----LAAARNPEN 226
 DB 181 -IDALPPGAFAGQLSRLDLTSNRLATLAPD--PLFSRGRDAEASPAVLVSFGNPLH 237
 QY 227 CVCPLSWFGPWVRESHVTLASPEETR-CHFPKNAGRLLELDYADFQCPATTTATVPT 285
 DB 238 CANCELMLR-----RLARPDDLETCASPGLAGRYFWAVPEGEFSC----- 278
 QY 286 TRPVREPTALSSSLAPTWSLPTAPT---EAPSPSTAPPTVGPVPQ-----PQDCPP 336
 DB 279 -----EPPLIARHTQRLWLLEGQRATLRCALGDPAPTWHVWGPDDRLVGNSSRARAFP 332
 QY 337 STCLNGGTCHLGRHHLACL-PEGFTGLYCE-----SOMGQGRTPSPPTVTPR 384
 DB 333 NGTLEIGTVGADGAGGYTCIATNPAGEATARVELRLVIALPHGNGSSAEGRPGPSIAAS 392
 QY 385 PPRSL-----TLGIEP---VSPTSLRVGLQRYLQSSVQ-LRSLRLTYRNLSPGDKRLVTL 436
 DB 393 ARTAAGEGTESEPAVQVTEVTATSLVSWGPGPADPVMWFQIQYN--SSEDETLYR 450
 QY 437 RLPASLAETVTLRNPATYSVCMPLGPGRPVEGEA-----CGEAHTPPAVHSHAPV 491
 DB 451 IVPASSHHFLKHLVFGADYDLCLALSAPAGSDLTATRLGCAHFTSLPASPLCHALQ 510
 QY 492 TQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAQAQDKGVGPGAGPLELEG 551
 DB 511 AHVILGTLTV-----AVGGVLAALLVFTVALLV-RERG-----AGNRLPLKLSH 555
 QY 552 VKVPLEPGPKAT 563
 DB 556 VQSQTNGGPGSPT 567
 RESULT 9
 ID LRFNA MOUSE STANDARD; PRT; 636 AA.
 AC Q80XU8; Q3TOG8; Q8K3C4;
 DT 29-MAR-2005, integrated into UniProtKB/Swiss-Prot.
 DT 01-JUN-2003, sequence version 1.

DT 18-APR-2006, entry version 8.
DE 12 days embryo embryonic body between diaphragm region and neck cDNA,
DE RIKEN full-length enriched library, clone:9430023110
DE product:Fibronectin leucine rich transmembrane protein 2, full insert
DE sequence.
GN Name=Map4k5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Embryonic body between diaphragm region and
RC neck;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning.";
RA Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Embryonic body between diaphragm region and
RC neck;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Cluttenbuck D.R.,
RA Crowe M.P., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Paulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Humineck L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottaqui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schombach C., Sekiguchi K., Sempile C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugita R., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusica V., Quackenbush J.,
RA Wuklestet C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki K., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Embryonic body between diaphragm region and
RC neck;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core team) and the FANTOM Consortium;
RT "Antisense transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Embryonic body between diaphragm region and
RC neck;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaio I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusica V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Haehizume W., Imotani K., Iehli Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Embryonic body between diaphragm region and
RC neck;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Iehli Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaio I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Maehima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Embryonic body between diaphragm region and
RC neck;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Embryonic body between diaphragm region and
RC neck;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitesunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakauchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-Format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Embryonic body between diaphragm region and
RC neck;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AK136973; BAE23193.1; -, mRNA.
DR MGI; MGI:1925503; Map4k5.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPRO03961; FN_III.
DR InterPro; IPRO08957; FN_III-like.
DR InterPro; IPRO01611; LRR.
DR InterPro; IPRO00483; LRR_C.
DR InterPro; IPRO00372; LRR_CYS_N.
DR InterPro; IPRO03591; LRR_TYP.
DR InterPro; IPRO13090; Phospholip_A2_AS.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00560; LRR_1; 9.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01462; LRRNT; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00369; LRR_TYP; 1.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00013; LRRNT; 1.
DR PROSITE; PS00853; FN3; 1.
DR PROSITE; PS00119; PA2_ASP; UNKNOWN 1.
KW Leucine-rich repeat; Membrane; Repeat; Transmembrane.
SQ SEQUENCE 634 AA; 71069 MW; 097196FE607D8085 CRC64;

Query Match 10.9%; Score 341; DB 2; Length 634;
Best Local Similarity 23.1%; Pred. No. 4.2e-11;
Matches 143; Conservative 85; Mismatches 238; Indels 154; Gaps 19;

QY 4 RVPLLPLLLLLALGPGVQ-----GCPGCGCQSQPQTVFCTARQCTTVPRDVPDVTGLY 58
DB 11 RGAFILKFWLIIISGLYLQVSKLLACPSVCRCDR-NFVYCNERSLTSVPLGPEGVTIVLY 69
QY 59 VF-----ENGMFLDASSF 72
DB 70 LHNQINNAGFPALHNQVSHVTVLYGNLDFPNNLPKNRVVLHLENNIOTISRAAL 129
QY 73 AGLPGLQLDLSONQIASLRP-----RLLLDLSHNSLALAPGI---LDTANVEA 121
DB 130 AQLKLEELHLDNSISTVGDEGAFRAISLKLFLSKNHLSSVPVGLPVDLQELRVD 189
QY 122 LRLA---GLGLQQLD-----EGLFSRLNHLDLVDSDNQLERVPVVI 160
DB 190 NRIAVISDMAFQNLTSRLERLVDGNLNTKNGIAEGTFSHLTCLKBFSIVRNSLSHPDPL 249
QY 161 RGLRGHTRLRAGNTRIAQLRPEDLAGLALQELDVNSLSLOALPGDSLGLPRLRLAA 220
DB 250 PGTH-LIRLYLDQN-QINHLPTAFANLRKLERLDISNNQLRMLTGVDFDHLNLKQLTA 307

QY 221 ARNPENCPLSWFGFVWRSHVTLASPEETCHPPKKNAGRLLELDYADFCCPATTITT 280
DB 308 RNNPFCDCSIRKWTWELKYIPSSL-NVRGFCQGEQVGRGMAVRLNNLLSCPTTPG 366
QY 281 ATVPTRPVVREPTALSSSLATWLSPTAPATEAPSPSTAPPTVGVPPQDQCPSPSTCL 340
DB 367 LPVFTAP-----STVSTTQSPTL-----SVPSRGSVPPTPSKLPIDW 411
QY 341 NGGTCHLGTRHHLACLCPGFTGLYCESQMGQGTSPPTVTPRPPRSUTLGLIEPVSPIS 400
DB 412 DG-----RERVTPPISERIQLSIHFNVDTS 436
QY 401 LRVGLQRYLQSSVQLRSRLTYRNLSPGDKLVLTLRLPASLAEY-TVTLRNPATYSVC 459
DB 437 IQVSMLSLFTVMAYKLTWQMGHSLVGG-----IVQERIVSGEKQHLUSLVNLEPRSTRYIC 492
QY 460 VNPLOGRGPVEGEAE-CGEAHTPPA-----VHSNHAPVTOAREGNLPLLIAPALAAVL 511
DB 493 LVPLDAFNRYTVEDTICSEATTHASVLYNNGSNNTASSHEQTTSMSG-S-PFLLAGLIGGAV 551
QY 512 LAALAAVGAAYC---VRRGR 528
DB 552 IFVLVLLSVFCWHMHKGR 571

RESULT 12
Q8BLUO MOUSE
ID Q8BLUO MOUSE PRELIMINARY; PRT; 660 AA.
AC Q8BLUO;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 21-JUN-2006, sequence version 1.
DT 01-MAR-2003, entry version 30.
DE Adult male aorta and vein cDNA, RIKEN full-length enriched library,
DE clone:A530098L04 product:LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN
DE FLRT2 homolog (10 days neonate cerebellum cDNA, RIKEN full-length
DE enriched library, clone:6530421A03 product:Fibronectin leucine rich
DE transmembrane protein 2, full insert sequence) (Fibronectin leucine
DE rich transmembrane protein 2).
DE Name:Flrt2; Synonyms:Map4k5;
GN Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Cerebellum;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Cerebellum;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambeesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Belsel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo C., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummelnick L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Karapin A., Katoh M., Kawasaki Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,

RA Motagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA Nilsson Y., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlancho V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J.C., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sadelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Sano S., Seesa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yeghi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmer S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome."; Science 309:1559-1563(2005).
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Cerebellum;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the PANTOM Consortium;
RT "Antisense transcription in the Mammalian Transcriptome."; Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Cerebellum;
RX MEDLINE=22354683; PubMed=12456851; DOI=10.1038/nature01266;
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Macsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Clothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer J.C.,
RA Gaasterland T., Gariboldi M., Glessi C., Godzik A., Gough J.,
RA Grimmer S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawagawa Y., Kedziercki R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kugawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yaeunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs"; Nature 420:563-573(2002).
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Cerebellum;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bash G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Tovo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Cerebellum;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Cerebellum;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Washiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Kato H., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RT Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. Metallothionien-TGF alpha model.
RX 10 month old virgin mouse. Taken by biopsy.;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.S., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Query Match 10.9%; Score 341; DB 2; Length 660;
Best Local Similarity 23.1%; Pred. No. 4.4e-11;
Matches 143; Conservative 85; Mismatches 238; Indels 154; Gaps 19;

QY 4 RVPLELLPLLLALGPGVQ-----GPGSGCCSQPOTVFCTARQGTTPRDVPPDPVGLY 58
Db 11 RGAFILKFWLIIISGLYLQVSKLLACPSVCRCDR-NFVYCNERSLSVPLGPEGVTVLY 69
QY 59 VF-----ENGITMLDASSF 72
Db 70 LHNQINNAGFPALHNVOQSVHTVYVYGNQDLDFPNLPKNVRLVHLQENNIQTISRAAL 129
QY 73 AGLPGLQLDLSONQIASRLP-----RLLLDLSHNSLLALBPGI---LDTANVEA 121
Db 130 AQLLKLEELHLDNSISTGVGEDGAFREAISLKLFLSKNHLSSVPGVLPVDLQELRVDE 189
QY 122 LRLA---GLGLQOLD-----EGLFSRLRNHLDDVSDNQLERVPVPI 160
Db 190 NRIAVISDMAFONLTSRLERLVDGNLLTNKGIAEGTFSHLTCLKFISIVRNSLSHPDPL 249
QY 161 RGLRGITRLRLAGNTRIAQLRPDLAGLAAQLBQELDVSNLSLOALPGDLSGLFPRLLAA 220
Db 250 PGTH-LIRLYLDN-QINHILPTAFANLKLRLDYSNNQLRMLTQGVFDHLSNLKQLTA 307
QY 221 ARNPFNCVPLSFGFWMVRESHTVLTASPEBTRCHFPKNAGRLLLELDVDFGCPATTTT 280
Db 308 RNNPWFCDCSIKVTEWLKIPSSL-NVRGFMCGEQRVGMVARELNWNLSCPTTTPG 366
QY 281 ATVPTTRPVVREPTALSSSLAPTWSLPTAPATEAPSPPTAPTVGPVQPOCPSPSTCL 340
Db 367 LPVFTAP-----STVSPITQSPTL-----SVPSRSGSVPPAPTPSKLPTIPDW 411
QY 341 NGCTCHLGTTHHLACLCPGFTGLYCESQMGQTRSPPTVTPRPSRLTLGIEPVSPTS 400
Db 412 DG-----RERVTPPISERIQLSHFVNDTS 436
QY 401 LRVGLQRYLQSSVOLRSRLTYRNLSSGDPKRLVTLRLPASLAEX-TVTOLRNPATYSVC 459
Db 437 IQVSWLSLFTVMYKLTWVKGHSLVG-----IVQERIVSGEKQHLVNLPRSTYRIC 492
QY 460 VMLPGFGRVPEGEA-CGEATTPPA-----VHSNHAPVTOAREGNLPLLIAPALAAVL 511
Db 493 LVLPDAPNRYTVEDTICSEATHTASVYLNNGSNTASSHEQTTSMSGSP-PLLAGLIGGAV 551
QY 512 LALAAGVAAAYC---VRRGR 528
Db 552 IFVLVLLSVFCVHMKKGR 571

RESULT 13
LRC24 MOUSE
AC QBHAI;
DT 04-APR-2006, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2003, sequence version 1.
DT 30-MAY-2006, entry version 33.
DE Leucine-rich repeat-containing protein 24 precursor.
GN Name=LRC24;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
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RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
RX STRAIN=C57BL/6J; TISSUE=Cerebellum, and Olfactory bulb;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carrinci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Imbondato A., Apweiler R., Attalaya R.N., Bailey T.L., M.,
RA Bansal K., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T., Gojobori T., Green R.E., N.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hilt D., Huminicki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasaki Y., Kelson J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareu L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., K.,
RA Matsuoka H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schoenbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
RA Tammaja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Tesard R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Lida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
CC -!- SUBCELLULAR LOCATION: Membrane, single-pass membrane protein
CC (Potential).
CC -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
CC domain.
CC -!- SIMILARITY: Contains 7 LRR (leucine-rich) repeats.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC
CC EMBL; AK049678; BAC33419.1; -; mRNA.
CC EMBL; AK078176; BAC37163.1; -; mRNA.
CC UniGene; Mm.289666; -.
CC HSSP; Q9BZR6; I02N.
CC
CC Ensembl; ENSMUSG00000033707; Mus musculus.
CC MGI; MGI:3605040; Lrrc24.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR013098; Ig_1-set.
CC InterPro; IPR003599; Ig_sub.
CC InterPro; IPR003598; Ig_sub2.
CC InterPro; IPR001611; LRR.
CC InterPro; IPR000483; LRR_C.
CC InterPro; IPR003591; LRR_typ.
CC Pfam; PF07679; I-set; 1.
CC Pfam; PF00560; LRR_1; 4.
CC Pfam; PF01463; LRRCT; 1.
CC PRINTS; PR00019; LEURICHRPT.
CC SMART; SM00409; IG; 1.
CC SMART; SM00408; IGc2; 1.
CC SMART; SM00369; LRR_TYP; 3.
CC SMART; SM00082; LRRCT; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
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KW Glycoprotein; Immunoglobulin domain; Leucine-rich repeat; Membrane;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 521 Leucine-rich repeat-containing protein
FT 24.
FT /FTId=PRO_0000231597.
FT TRANSMEM 414 434 Potential.
FT REPEAT 57 80 LRR 1.
FT REPEAT 81 104 LRR 2.
FT REPEAT 106 128 LRR 3.
FT REPEAT 130 152 LRR 4.
FT REPEAT 153 176 LRR 5.
FT REPEAT 178 200 LRR 6.
FT REPEAT 252 273 LRR 7.
FT DOMAIN 268 371 Ig-like C2-type.
FT COMPIAS 435 440 Poly-Arg.
FT CARBOHYD 91 91 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 342 342 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 371 371 N-linked (GlcNAc...) (Potential).
FT DISULFID 289 353 By similarity.
SQ SEQUENCE 521 AA; 56334 MW; 3D1E4BEE302284A6 CRC64;
Query Match 10.8%; Score 339; DB 1; Length 521;
Best Local Similarity 27.0%; Pred. No. 4.5e-11;
Matches 149; Conservative 66; Mismatches 217; Indels 120; Gaps 21;
QY 1 MCSRVPILLLPL---LILLALRGV---QCPSGCGCSPQTVFCTARQCTTVPRDVPDP 53
DB 1 MAURAPTLILLGLLLPLLPPLPRATCPAACRC-YSATVECGALRLRVVPPGIPGP 59
QY 54 TVGLYFENGITMLDASSFAGLPGQLQLDLSQNOIASLR-----LPRILLDLSHNSLL 107
DB 60 TQTLFLODNSIAHLEQGSFLAPLAALRHLYLHNTLRALSGAFRAQPRLLLELATGNRLR 119
QY 108 ALSPG-ILDTANVEARLAGLGLQDLDEGLFSRLNLHLDVSDNQLRVPVIRGLRL 166
DB 120 GLRGGAFLVGLRVLYLAGNQLAKLLDFTFLHPLRLQLHLQENST----- 167
QY 167 TRLRLAGNTRIAQLRPEDLAGLAALQELDVNSLSIQALPGDLSGLFPRLLRLAAARNPF 226
DB 168 -----LLEQALAGLSLLALLDLSRNQLGTISKEALQPLSSQVRLRTENPMR 215
QY 227 CVCPLSWFGVWRESHTVLASPETR--CHFFPKNAGRLLELDYADFQCPATTTATVP 284
DB 216 CDCAHLWLSWKEGGRLLSRDKKITCAEPRLALQSLLEVSGLSIC-----IP 267
QY 285 TTRPVREPTALSSSLAPTWSLSTAPATEAPSPPTAPPTVGPVQPDCCP--STCLNG 342
DB 268 PSVNV--EPPEFTANLGED-LQVACQASGYQP-----LVVWRKVPQPRDGKPOAQLEG 320
QY 343 GTCHLG-----TRHILACLPEGETGLY-CESQMGCGTRPSPTVTPRPPR 387
DB 321 GAPGLGGHTRDTCGMLFTNTTLA-----HAGRYECEAANAGGARVFHLLVNASR 374
QY 388 SLTLGI-EPVSPTSRLVGLQRYLQSSVQLRSRLRTYRNLSGPDKRLVTL----- 436
DB 375 QSQQLPDPQAPATRPVGHFPEQHEAGSMAPFALGLATQTATTAIALLATALLLAAMIC 434
QY 437 -----RLPASLAEYF-----VTQLRPNATYSVCMV-----PLGPGRVPE 470
DB 435 RRRRRKKVPAPSGEGTLFVNDYSDGCTPQAELELRDDHGHMFVDRSKPLFPFVLP- 493
QY 471 GEACGEAHTPP 482
DB 494 -EEA--PEHNPP 502

RESULT 14
Q4SGV9 TETNG
ID Q4SGV9 TETNG PRELIMINARY; PRT; 655 AA.
AC Q4SGV9;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.

DT 27-JUN-2006, entry version 8.
DE Chromosome 14 SCAR14590, whole genome shotgun sequence. (Fragment).
GN ORFNames=GSTENG00018451001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bounneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellan S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Gerardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: CAAE01014590; CAG00123.1; -; Genomic_DNA.
DR InterPro: IPR003961; FN III
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_C.
DR InterPro: IPR000372; LRR_Cys_N.
DR InterPro: IPR003591; LRR_Typ.
DR Pfam: PF00041; fn3; 1.
DR Pfam: PF00560; LRR_1; 8.
DR Pfam: PF01463; LRRCT; 1.
DR Pfam: PF01462; LRRNT; 1.
DR PRINTS: PR00019; LEURICHRPT.
DR SMART: SM00369; LRR_TYP; 1.
DR SMART: SM00082; LRRCT; 1.
DR SMART: SM00013; LRRNT; 1.
DR PROSITE: PS50853; FN3; 1.
FT NON_TER 1 1
FT NON_TER 655 655
SQ SEQUENCE 655 AA; 72743 MW; 8EF35565F5B1B126 CRC64;
Query Match 10.8%; Score 338; DB 2; Length 655;
Best Local Similarity 25.3%; Pred. No. 6.5e-11;
Matches 160; Conservative 78; Mismatches 206; Indels 188; Gaps 31;
QY 7 LLLPLLLALLGPGVCGCSCQSPQTVFCTARQCTTVPR----- 48
DB 13 LTVTLSQLVRLRGA--SCPQECRCDN-TFYCNERSLTSVPLGIQGYKVLFLHNQINN 70
QY 49 -----DVPPDTGLYVFPENGITMLDASSFAGLPGQL 80
DB 71 AGFPVELLHLASVETVHLYGNQLDEFFINLPKNTRVLHLQENNIQTISRAALQTLREE 130
QY 81 LDLSQNOIASLRPLR-----LILLDLSHNSLLALEPGI---LDTANVEARLAGL- 128
DB 131 LHLDDNSISTVGVEEAGFRAVSLKLLFLTKNHLSSVPIGLPEELRLDENRIAVIAE 190

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QY 129 -----LOOL-----DEGL-----PSRLNHLVDSDNQLERVPVPIGLRLTR 168
DB 191 EAFQNYRLQRLLDGNLLTDEGAPGTFODLVNLRELALARNSLTFPPPLPG-RALFR 249
QY 169 LRLAGNTRIAQLRPEDLAGLAALQELDVSNLSQAL-PGDLGLFPLRLRLAAARNPNC 227
DB 250 LSLQEN-QIDQIPVAAFAGLHRLKLDVSNQLSLTQGVFEG-LNALHMLVNNPWR 307
QY 228 VCLPSNFGPWRVSHVTLASPEETR---CHFPKPNAGRLLELDYADFGCPATTTATVP 284
DB 308 DCAVKWVWVLR---SLPASVNAFGVQCPKVRGMAIRELTLVDVIECP----- 354
QY 285 TTPVVPREPALSSSLAPTHLSATAPATAPSPSTAPPVGPVQPDQCPSTCLNGGT 344
DB 355 -----PGAGS-----PSW---PFLRST-PPPPPTTAPTATTAGSTAITPP----- 391
QY 345 CHLGRTHRLACLCEGFTGLYCDSQMGQGRPSPT---PVTPRPRS--LTGIBPVSP 398
DB 392 -----IPYFES-----SSPPVPSLRNPPGLPPYEDPLQIYFHVNS 430
QY 399 TSLRVGLQRYLOGSSVQLRSLRITY-----RNLSPDKRLVTLRLPASLAETVTLQRP 452
DB 431 SNIEVSWASYF---TVTAYKVTWVKRGQQTNEGPRERTV---GGDQRISLGNLEP 481
QY 453 NATYSVCWPLG-----PGRVPEGEACCEATPPAVHS-----NHAPVQAREG-NLP 500
DB 482 RSVYRICVHVLDLTINSYRPOE---DTLCSSEARTKAAASTKAPGRDHAP---QEGIHST 533
QY 501 LLTAPALAAVLLAALAAVGAAYC---VRRGRA 529
DB 534 LMWAGIIGGAVLLVATLGLFCWYVHRKSA 565

RESULT 15
Q6A073 MOUSE
ID Q6A073 MOUSE PRELIMINARY; PRT; 637 AA.
AC Q6A073;
DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2004, sequence version 1.
DT 27-JUN-2006, entry version 19.
DE MKIA0405 protein (Fragment).
GN Name=Map4k5; Synonyms=Flt2, mKIAA0405;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX PubMed=15368895; DOI=10.1093/dnares/11.3.205;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,
RA Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT IV. The complete nucleotide sequences of 500 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 11:205-218(2004).
CC -----
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CC -----
DR EMBL: AK172945; BAD32223.1; -; mRNA.
DR Ensembl: ENSMUSG00000047414; Mus musculus.
DR MGI: MGI:3603594; Flt2.
DR MGI: MGI:1925503; Map4k5.
DR InterPro: IPR003961; FN III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR016111; LRR.
DR InterPro: IPR000483; LRR_C.
DR InterPro: IPR000372; LRR_cys_N.
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DR InterPro: IPR003591; LRR typ.
DR InterPro: IPR013090; Phospholip_A2_AS.
DR Pfam: PF000411; fn3; 1.
DR Pfam: PF00560; LRR_1; 9.
DR Pfam: PF01463; LRRCT; 1.
DR Pfam: PF01462; LRRNT; 1.
DR PRINTS: PR00019; LEURICHRPT.
DR SMART: SM00369; LRR_TYP; 1.
DR SMART: SM00082; LRRCT; 1.
DR SMART: SM00013; LRRNT; 1.
DR PROSITE: PS00853; FN3; 1.
DR PROSITE: PS00119; PA2 ASP; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 637 AA; 71302 MW; 9577AD980D67162F CRC64;

Query Match 10.6%; Score 332; DB 2; Length 637;
Best Local Similarity 23.2%; Pred. No. 1.4e-10;
Matches 142; Conservative 81; Mismatches 233; Indels 156; Gaps 19;

QY 7 LLLPLLLLLALGPGVQCGSCGCSQSQPQVFTARQGTTPRDPVDPDTVGLIYF----- 60
DB 3 LYLQVSKLLA-----CPSCVRCRDR-NFYVCNERSLTSVPLGIPGVTVLYLHNQINN 54
QY 61 -----ENGITWLDASSFAGLPGQL 80
DB 55 AGFPAELHNVSQVHTVLYGNQDLDEFPNMLPKNVRVHLQENNIQTSRAALAQLKLEE 114
QY 81 LQLSQNIQIASLRP-----RLLLDLSHNSLLALEPGI---LDTANVEALRLA---G 126
DB 115 LHLDDNSISTVGVEDGAFREAIKLLFLSKNHLSSVPVGLPVDLQELRVDENRIAVISD 174
QY 127 LGLQLD-----EGLFSRLNHLHDLDVSDNQLERVPVPIGLRLTR 168
DB 175 MAFQNLTSRLERLIVDGNLNTNKGIAEGTFSHLTKKEFSIVRNSLSHPDPDLPGTH-LIR 233
QY 169 LRLAGNTRIAQLRPEDLAGLAALQELDVSNLSQALPGDLGSLFPPLRLAAARNPNCV 228
DB 234 LYLQDN-QINHLPLTAFANRLKLERLDISNNQLRMLTQGVFDHLSNLKQLTARNNWFCD 232
QY 229 CPLSNFGPWRVSHVTLASPEETRCHFPKPNAGRLLELDYADFGCPATTTATVPTTRP 288
DB 293 CSIKVTEWMLKYPSSL-NVRGFMCGQPGVGRMAVRELNMNLLSCTTTTGLPVFTTAP 351
QY 289 VREPTALSSSLAPTWLSPATAPATEAPSPSTAPPVGPVQPDQCPSTCLNGGTCHLG 348
DB 352 -----STVSPITQSPTL-----SVSPSRGSPVPAPTPSKLTPIPDWDG----- 390
QY 349 TRHHLACLCEGFTGLYCDSQMGQGRPSPTPVTTPRPSRLTGLIEFVSPSTSLRVGLQRY 408
DB 391 -----RERVTPPISERIQLSIHFVNDTISIQVSWLSL 421
QY 409 LQSSSVQLRSLRLTYRNLSPDKRLVTLRLPASLAAY-TVTLRPNATYSVCVMPGPGCR 467
DB 422 FTWYAKYLTWVKMCHSLVGG---IVQERIVSGEKHLSLVNLEPSTRYICLVPLDAFN 477
QY 468 VPEGEA-CGEAHTPPA-----VHNSHAPVTOAREGNLPLLIAPALAAVLLAALAAVG 519
DB 478 YRTVEDTICEATTHASYLNNGSNTASSHEQTTSMSG-S-PFLLAGLIGGAVIFVLVLL 536
QY 520 AAYC---VRRGR 528
DB 537 SVFCWHMHKKGR 548
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Search completed: January 28, 2007, 17:34:01

Job time : 379 secs

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GenCore version 6.2
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OM protein - protein search, using sw model

Run on: January 28, 2007, 17:26:16 ; Search time 44 Seconds
(without alignments)
1307.673 Million cell updates/sec

Title: US-10-677-669-69
Perfect score: 3135
Sequence: 1 MCSRVPLLLPLLLLLLALPGP.....PLMGFPGLQSPHAKPYI 598

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR 80.*
1: piri.*
2: piri2.*
3: piri3.*
4: piri4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	322	10.3	605	2 JC5239	insulin-like growth
2	302	9.6	605	2 A41915	insulin-like growth
3	282	9.0	626	1 NBHUIA	platelet glycoprot
4	281.5	9.0	603	2 JC1282	insulin-like growth
5	278.5	8.9	603	2 JC6128	insulin-like growth
6	278	8.9	1531	2 T42218	slit-1 protein hom
7	264.5	8.4	420	2 A53531	oncofetal trophobl
8	261	8.3	1523	2 T13953	MEGF5 protein - ra
9	255.5	8.1	1469	2 B36655	slit protein 2 pre
10	255.5	8.1	1480	2 A36655	slit protein 1 pre
11	251	8.0	622	2 JC7973	synleurin - huma
12	243.5	7.8	312	1 NBHUIA	leucine-rich alpha
13	240	7.7	560	2 A60164	platelet membrane
14	237	7.6	707	2 JC7763	neural leucine-r
15	231	7.4	1025	2 T42626	secreted leucine-r
16	222.5	7.1	1536	2 A34901	lysine carboxypept
17	214.5	6.8	1535	2 S46224	peroxidase - fru
18	212.5	6.8	361	2 A53860	chondroadherin pre
19	210.5	6.7	4302	2 A38971	polycystic kidney
20	209	6.7	1091	2 A58532	glial cell membran
21	208.5	6.7	382	2 T39068	proline-arginine-
22	200	6.4	653	2 T25194	hypothetical prote
23	199	6.3	1328	2 T23007	hypothetical prote
24	194.5	6.2	789	2 T28715	hypothetical prote
25	194.5	6.2	1355	2 T28715	hypothetical prote
26	193.5	6.2	421	2 T46266	hypothetical prote
27	193.5	6.2	721	2 E70766	hypothetical prote
28	192.5	6.1	575	2 T29972	hypothetical prote
29	189	6.0	369	2 S20811	proteoglycan I - m

30	189	6.0	369	2	S32793	biglycan precursor
31	189	6.0	839	2	T04859	extensin homolog F
32	188.5	6.0	440	2	A47530	oligodendrocyte-my
33	186	5.9	440	2	A39613	oligodendrocyte-my
34	184	5.9	368	1	BGHUN	biglycan precursor
35	183	5.8	662	2	S42799	garp precursor - h
36	182	5.8	369	2	S32559	biglycan precursor
37	181.5	5.8	357	2	S24317	decorin precursor
38	177.5	5.7	2493	2	A55481	adenylate cyclase
39	176.5	5.6	1495	2	T31434	densin-180 - rat
40	175	5.6	343	2	A41748	lumican precursor
41	173	5.5	925	2	JC2033	G protein-coupled
42	172.5	5.5	359	1	NBHUC8	decorin precursor
43	172	5.5	1134	2	T04587	hypothetical prote
44	170.5	5.4	2145	2	JC4747	adenylate cyclase
45	170	5.4	907	2	JE0176	orphan G protein-c
46	169.5	5.4	760	2	T06291	extensin homolog T
47	169	5.4	354	2	A55454	decorin precursor
48	169	5.4	839	2	F75518	hypothetical prote
49	168.5	5.4	907	2	JG0193	G protein-coupled
50	167	5.3	800	2	S37387	internalin A precu
51	167	5.3	1112	2	T10504	disease resistance
52	166.5	5.3	549	2	T41744	hypothetical prote
53	166.5	5.3	800	2	AB1129	Internalin A limpo
54	165.5	5.3	360	2	S06280	decorin precursor
55	165.5	5.3	526	2	C84552	hypothetical prote
56	165.5	5.3	1256	2	S60461	gene flightless-I
57	165.5	5.3	1268	2	A49674	flightless-I homol
58	165	5.3	994	2	H96510	probable disease r
59	163.5	5.2	786	2	T01456	extensin homolog F
60	162	5.2	242	2	T14791	hypothetical prote
61	161	5.1	559	2	T42998	Ras-binding protei
62	161	5.1	682	2	A49121	cell-surface molec
63	161	5.1	682	2	A43318	connectin precursor
64	160.5	5.1	2910	2	T42214	otogelin - mouse
65	160	5.1	744	2	E86255	hypothetical prote
66	159.5	5.1	1112	2	T00552	hypothetical prote
67	159	5.1	572	2	T30947	protein AC7.2 (imp
68	159	5.1	613	2	A88684	hypothetical prote
69	159	5.1	702	2	T21148	hypothetical prote
70	159	5.1	1119	2	AD1822	leucine-rich-repea
71	158.5	5.1	738	2	T19938	hypothetical prote
72	158	5.0	1086	2	T15864	hypothetical prote
73	158	5.0	3570	2	T45025	mucin MUC5B, trach
74	156.5	5.0	360	2	I47020	decorin - rabbit
75	156.5	5.0	980	2	H46432	probable receptor-
76	156	5.0	354	2	S29145	decorin precursor
77	156	5.0	584	2	T23841	hypothetical prote
78	155.5	5.0	903	2	T00705	N-chimerin homolog
79	155.5	5.0	1334	2	T50568	probable multi-dom
80	155	4.9	961	2	T23395	hypothetical prote
81	154.5	4.9	1013	2	T10659	probable serine/th
82	154.5	4.9	1143	2	T10636	hypothetical prote
83	154.5	4.9	1132	2	T48499	receptor-like prot
84	154.5	4.9	1495	2	S06255	transcription co-r
85	153.5	4.9	864	2	T08575	protein kinase hom
86	153.5	4.9	894	1	A41527	protein-tyrosine k
87	153	4.9	699	2	C43674	US4 protein - huma
88	152	4.8	786	2	T08664	Toll protein-like
89	151.5	4.8	695	1	JN0898	folliculin recept
90	151	4.8	540	2	T12704	leucine-rich prote
91	151	4.8	1389	2	T13852	gene wheeler prote
92	150.5	4.8	695	1	QRHUT	folliculin recept
93	150.5	4.8	1109	2	T18536	receptor-like prot
94	150	4.8	1134	1	A29944	chaoptin precursor
95	149.5	4.8	224	2	T32185	hypothetical prote
96	149.5	4.8	696	2	JC7361	folliculin recept
97	149	4.8	1025	1	A57676	protein kinase Xa2
98	149	4.8	1143	2	B84431	probable receptor
99	149	4.8	2357	2	A59249	class VII unconven
100	148.5	4.7	375	2	S05390	fibromodulin precu
101	148.5	4.7	610	2	T23836	hypothetical prote
102	148.5	4.7	680	2	T19939	hypothetical prote

103	148.5	4.7	890	2	C96654	hypothetical prote	176	136	4.3	4957	2	T03455	ALR protein - huma
104	148.5	4.7	964	2	T49038	hypothetical prote	177	135.5	4.3	427	2	JC4915	ags protein precu
105	148.5	4.7	1115	2	S40241	G protein-coupled	178	135.5	4.3	499	2	D83333	hypothetical prote
106	148	4.7	338	2	S52284	lumicon, secretory	179	135.5	4.3	1124	2	B84742	probable receptor-
107	148	4.7	1188	2	S49915	extensin-like prot	180	135.5	4.3	5262	2	T03454	ALR protein - huma
108	147.5	4.7	316	2	A41781	proteoglycan-Lb -	181	135	4.3	601	2	S56144	SH3 domain binding
109	147.5	4.7	1385	2	T13087	tlr protein - frui	182	134.5	4.3	613	2	T15489	hypothetical prote
110	147	4.7	1964	2	T09059	notch4 - mouse	183	134.5	4.3	847	2	F96531	hypothetical prote
111	147	4.7	2414	2	A54277	transcription adap	184	134.5	4.3	1039	2	T22117	hypothetical prote
112	146.5	4.7	382	2	T04260	hypothetical prote	185	134	4.3	530	2	A45690	transactivator EBN
113	146.5	4.7	925	2	C84538	probable LRR recep	186	134	4.3	656	2	B47096	hylB homolog - Str
114	146.5	4.7	1408	2	S16148	gene serrate prote	187	134	4.3	886	2	T40734	probable adenylate
115	146	4.7	369	2	C83434	translocation prot	188	133.5	4.3	277	2	S25770	RSP-1 protein - mo
116	145.5	4.6	380	2	S71876	fibromodulin - chi	189	133.5	4.3	384	2	A41710	promastigote surfa
117	145.5	4.6	886	2	S29605	glycoprotein 350/2	190	133.5	4.3	1068	2	H96769	hypothetical prote
118	145.5	4.6	2142	2	B35098	MHC class III hist	191	133	4.2	576	2	T36729	probable serine/th
119	145	4.6	458	2	T19941	hypothetical prote	192	133	4.2	852	2	I51259	tyrosine kinase C
120	145	4.6	679	2	T20713	hypothetical prote	193	133	4.2	932	2	T48489	receptor-like prot
121	145	4.6	694	2	JC2237	foliitropin recept	194	133	4.2	1257	2	A88536	protein B053.5 [i
122	145	4.6	1839	1	OYBYK	adenylate cyclase	195	133	4.2	4391	2	A38096	perlecan precursor
123	144.5	4.6	486	2	B86460	hypothetical prote	196	132.5	4.2	463	1	A36479	milk fat globule m
124	144.5	4.6	2187	2	T30826	nascent polypeptid	197	132.5	4.2	2035	2	A40718	host cell factor C
125	144.5	4.6	3149	1	Q0BB8	BRP1 protein - hu	198	132	4.2	3164	1	WMBEH6	UL36 protein - hum
126	144	4.6	695	2	T45896	follicle stimulati	199	131.5	4.2	346	2	T46316	hypothetical prote
127	144	4.6	1019	2	C96519	probable disease r	200	131.5	4.2	890	2	T00800	disease resistance
128	144	4.6	3020	2	A43932	mucin 2 precursor,	201	131.5	4.2	1097	2	A29943	Toll protein precu
129	143.5	4.6	243	2	B41710	promastigote surfa	202	131.5	4.2	1286	2	A88396	protein M01B10.2 [
130	143.5	4.6	476	2	T27051	hypothetical prote	203	131	4.2	612	2	T10727	protein kinase Xa2
131	143.5	4.6	496	2	C96832	hypothetical prote	204	131	4.2	767	2	B84594	probable LRR recep
132	143.5	4.6	605	2	T50817	protein serine/thr	205	131	4.2	905	2	T00475	probable disease r
133	143.5	4.6	683	2	T24486	hypothetical prote	206	131	4.2	1095	2	T09575	smoothenin - human
134	142.5	4.5	1870	2	S37671	MHC class III hist	207	131	4.2	1095	2	G96746	hypothetical prote
135	142.5	4.5	1872	2	S36152	MHC class III hist	208	131	4.2	1196	2	T09356	brassinosteroid-in
136	142	4.5	661	2	I56258	RP105 - mouse	209	130.5	4.2	448	2	T27395	hypothetical prote
137	142	4.5	983	2	G84524	probable disease r	210	130	4.1	268	2	T19597	hypothetical prote
138	141.5	4.5	462	2	D84858	hypothetical prote	211	130	4.1	389	2	H86266	hypothetical prote
139	141.5	4.5	836	2	T46070	hypothetical prote	212	130	4.1	395	2	H75457	hypothetical prote
140	141.5	4.5	1029	2	T05050	protein kinase hom	213	130	4.1	768	2	T17462	disease resistance
141	141.5	4.5	1051	2	T13174	gp150 protein - fr	214	130	4.1	800	2	H84740	hypothetical prote
142	141	4.5	630	2	AC1129	Internalin B [limpo	215	129.5	4.1	315	2	T06806	proline rich prote
143	141	4.5	717	2	T33295	hypothetical prote	216	129.5	4.1	780	2	T00366	hypothetical prote
144	140.5	4.5	376	2	S55275	fibromodulin precu	217	129.5	4.1	861	2	A48825	Notch homolog Motc
145	140	4.5	277	2	T60122	rau-1 homolog - hu	218	129.5	4.1	912	2	A54423	hypothetical prote
146	140	4.5	474	2	S65763	chitinase [BC 3.2.	219	129.5	4.1	942	2	S23251	protein-tyrosine k
147	140	4.5	754	2	A85043	probable LRR recep	220	129.5	4.1	1173	2	I50620	basal transcrip
148	140	4.5	1029	2	T00712	protein kinase hom	221	129.5	4.1	1469	2	T09219	procr2 - chicken
149	139.5	4.4	333	2	T34555	hypothetical prote	222	129	4.1	371	2	S20075	basal transcrip
150	139.5	4.4	527	2	T75399	hypothetical prote	223	129	4.1	835	2	T05259	promastigote surfa
151	139.5	4.4	539	2	G70520	probable csp prote	224	129	4.1	910	2	B96770	probable disease r
152	139.5	4.4	4351	2	T00252	MEGF1 protein - ra	225	129	4.1	1037	2	B85089	hypothetical prote
153	139	4.4	581	2	A45531	insect-stage-speci	226	129	4.1	1064	2	B86465	receptor protein k
154	139	4.4	603	2	T24315	hypothetical prote	227	129	4.1	1232	2	T05322	probable Protein k
155	139	4.4	720	2	T02361	hypothetical prote	228	129	4.1	1329	2	A64828	hypothetical prote
156	139	4.4	1088	2	E86312	hypothetical prote	229	129	4.1	1342	2	B85614	cell division prot
157	139	4.4	2240	2	T37057	FlilA6.9 protein -	230	129	4.1	1342	2	G90750	cell division prot
158	138.5	4.4	342	2	A46743	probable multi-dom	231	129	4.1	1959	1	AGRT	agrin - rat
159	138.5	4.4	990	2	T14756	lumican precursor	232	129	4.1	2321	2	S78549	notch3 protein - h
160	138.5	4.4	1650	2	S53457	hypothetical prote	233	128.5	4.1	487	2	S42442	nuclear protein EB
161	138	4.4	630	2	C39930	dominant autoantig	234	128.5	4.1	677	2	H86208	protein P2295.26 [
162	138	4.4	858	2	T00258	hypothetical prote	235	128.5	4.1	727	2	C84534	hypothetical prote
163	138	4.4	1952	2	T48814	hypothetical prote	236	128.5	4.1	744	2	C84527	probable receptor-
164	137.5	4.4	1151	2	T18531	high molecular mas	237	128.5	4.1	835	2	T29634	hypothetical prote
165	137.5	4.4	4660	2	T42737	gp330 protein prec	238	128.5	4.1	1113	2	T00271	hypothetical prote
166	137	4.4	562	2	T34319	hypothetical prote	239	128.5	4.1	3968	2	A4265	trithorax homolog
167	137	4.4	695	2	JC1493	foliitropin recept	240	128	4.1	597	2	S72468	probable transcrip
168	137	4.4	788	2	AG0786	secreted effector	241	128	4.1	967	2	T48210	hypothetical prote
169	137	4.4	907	1	Q0BE21	membrane antigen g	242	128	4.1	1428	2	T08852	lustrin A - Calfo
170	137	4.4	4544	1	S02392	alpha-2-macroglobu	243	128	4.1	1914	2	T42635	tenascin Y precurs
171	137	4.4	4545	1	S25111	alpha-2-macroglobu	244	127.5	4.1	750	2	D86245	hypothetical prote
172	136	4.3	322	2	S72211	proteoglycan lb pr	245	127.5	4.1	1120	2	B86479	hypothetical prote
173	136	4.3	626	2	AE0123	probable antigenic	246	127.5	4.1	1784	2	C96615	hypothetical prote
174	136	4.3	692	2	A34548	foliitropin recept	247	127	4.1	327	2	S20074	promastigote surfa
175	136	4.3	1008	2	D84434	probable receptor-	248	127	4.1	773	2	T00502	probable receptor-

249	127	4.1	775	1	EDB11	immediate-early pr	322	121.5	3.9	432	2	E96712	unknown protein, 6
250	127	4.1	800	2	G84740	hypothetical prote	323	121.5	3.9	519	2	T07026	ethylene receptor
251	127	4.1	1366	2	T35985	probable large pro	324	121.5	3.9	635	2	T07794	ethylene receptor
252	127	4.1	1895	2	T06609	disease resistance	325	121.5	3.9	686	2	JC7569	Delta-4 protein -
253	127	4.1	1955	1	AGCH	agrin precursor -	326	121.5	3.9	760	2	F86387	probable Pro kinas
254	126.5	4.0	268	2	T45616	hypothetical prote	327	121.5	3.9	902	2	T00588	hypothetical prote
255	126.5	4.0	685	2	JC7570	Delta-4 protein -	328	121.5	3.9	1251	2	A57293	latent transformin
256	126.5	4.0	694	2	JC4301	folitropin recept	329	121.5	3.9	1409	2	T37188	presynaptic activi
257	126.5	4.0	862	2	T46289	hypothetical prote	330	121.5	3.9	2265	1	FNBO	fibronectin - bovi
258	126.5	4.0	999	1	S27756	receptor-like prot	331	121.5	3.9	2297	2	T34918	polyketide synthas
259	126.5	4.0	1091	2	S33596	protein-tyrosine k	332	121.5	3.9	2318	2	A54306	notch 3 protein -
260	126.5	4.0	1777	2	T34369	hypothetical prote	333	121.5	3.9	3530	2	A59266	unconventional myo
261	126	4.0	500	2	S49302	AWL218 protein -	334	121	3.9	306	2	T52340	cell wall-plasma m
262	126	4.0	865	2	A47282	calcium-binding pr	335	121	3.9	480	2	T00971	probable disease r
263	126	4.0	873	2	A47283	calphotin - fruit	336	121	3.9	485	2	A33647	sulfated surface g
264	126	4.0	996	2	F86410	protein F3M18.12	337	121	3.9	733	2	A45301	microtubule-associ
265	126	4.0	1152	2	T31911	hypothetical prote	338	121	3.9	1203	2	A49175	Notch B protein -
266	126	4.0	1820	2	A55494	latent transformin	339	121	3.9	1520	2	T00273	hypothetical prote
267	125.5	4.0	243	2	S13383	hydroxyproline-ric	340	121	3.9	2531	2	S18188	notch protein homo
268	125.5	4.0	548	2	AH1107	internalin H limpo	341	120.5	3.8	299	2	A35272	osteoinductive fac
269	125.5	4.0	635	2	T75477	hypothetical prote	342	120.5	3.8	753	2	JQ0532	Op protein - Kenne
270	125.5	4.0	764	2	A40077	thytotropin recept	343	120.5	3.8	821	2	AB1126	internalin, peptid
271	125.5	4.0	1003	2	T05898	hypothetical prote	344	120.5	3.8	855	2	T17460	disease resistance
272	125	4.0	350	2	S22456	hydroxyproline-ric	345	120.5	3.8	976	2	B84659	probable receptor-
273	125	4.0	476	2	A36478	surface glycoprote	346	120.5	3.8	976	2	T05897	protein kinase hom
274	125	4.0	783	2	T45899	receptor protein k	347	120.5	3.8	981	2	T50851	receptor protein k
275	125	4.0	818	2	F96586	hypothetical prote	348	120.5	3.8	987	2	T50850	receptor protein k
276	125	4.0	991	2	T52400	receptor-like prot	349	120.5	3.8	1118	2	A48292	mucin, tracheobron
277	125	4.0	1504	2	T49896	glycine/proline-ri	350	120.5	3.8	1152	2	A33183	microtubule-associ
278	125	4.0	2026	1	OYBY	adenylate cyclase	351	120.5	3.8	1722	2	E89753	protein p11C7.4 li
279	124.5	4.0	298	2	B35272	osteoinductive fac	352	120.5	3.8	1778	2	AF1116	internalin protein
280	124.5	4.0	756	2	T27642	hypothetical prote	353	120.5	3.8	3566	1	A40701	tenascin-X precurs
281	124.5	4.0	849	2	C97303	hypothetical prote	354	120	3.8	361	2	AH1469	internalin protein
282	124.5	4.0	910	2	G84648	probable disease r	355	120	3.8	376	2	S71558	probable cell wall
283	124.5	4.0	977	2	C96745	hypothetical prote	356	120	3.8	458	2	T31631	hypothetical prote
284	124.5	4.0	1223	2	E88451	protein K10D2.1 li	357	120	3.8	892	2	T09071	SH3 domains-contai
285	124.5	4.0	2176	2	T13806	toucan gene protei	358	120	3.8	962	2	T04124	receptor-like prot
286	124	4.0	496	2	D75261	conserved hypothet	359	120	3.8	1226	2	T20801	hypothetical prote
287	124	4.0	543	2	S35047	mucin JUL7 - human	360	120	3.8	1224	2	T40765	webl protein homol
288	124	4.0	574	2	T43556	Wiskott-Aldrich sy	361	119.5	3.8	267	2	S08314	cell wall glycopro
289	124	4.0	605	2	AG0123	probable antigenic	362	119.5	3.8	479	1	A31753	transcription fact
290	124	4.0	729	2	F70803	hypothetical prote	363	119.5	3.8	660	2	T45569	receptor protein k
291	124	4.0	766	2	B85440	receptor kinase-11	364	119.5	3.8	1048	1	XPBEA9	large structural p
292	124	4.0	978	2	E96787	protein T4012.5 li	365	119.5	3.8	1079	2	C96772	probable receptor
293	124	4.0	1011	2	T45718	receptor-kinase li	366	119.5	3.8	1166	2	F96598	protein F20N2.4 li
294	124	4.0	1472	2	B54774	ATP binding casset	367	119.5	3.8	1400	2	B70963	hypothetical prote
295	124	4.0	4135	2	T42629	tenascin-X - bovin	368	119.5	3.8	1596	2	A35927	190K DNA-binding p
296	123.5	3.9	380	2	T01281	probable leucine-r	369	119.5	3.8	1643	2	T14274	versican precursor
297	123.5	3.9	492	2	F86263	hypothetical prote	370	119	3.8	164	2	IS3641	mucin SAC - human
298	123.5	3.9	656	2	AE1479	probable cell surf	371	119	3.8	352	2	S49299	AWJL172 protein -
299	123.5	3.9	690	2	T41296	probable alcohol d	372	119	3.8	424	2	S27783	hypothetical prote
300	123	3.9	528	2	T15198	hypothetical prote	373	119	3.8	550	2	C75557	hypothetical prote
301	123	3.9	574	2	T38819	wiskott-aldrich sy	374	119	3.8	651	2	T42644	hypothetical prote
302	123	3.9	888	2	S23065	ufo protein - mous	375	119	3.8	660	1	Q0BE3	BHLFI protein - hu
303	123	3.9	1072	2	A37127	microtubule-associ	376	119	3.8	808	2	T23129	hypothetical prote
304	123	3.9	2591	2	T30288	pristinamycin I sy	377	119	3.8	864	2	D84740	hypothetical prote
305	122.5	3.9	303	2	S28364	hydroxyproline-ric	378	119	3.8	1006	2	T42731	atrophin-1 relate
306	122.5	3.9	415	2	T13435	hypothetical prote	379	119	3.8	1045	2	T41119	internalin- relate
307	122.5	3.9	592	2	D70863	hypothetical prote	380	118.5	3.8	222	2	H96711	hypothetical prote
308	122.5	3.9	699	2	T05225	extensin homolog F	381	118.5	3.8	400	1	A39822	leukosialin precu
309	122.5	3.9	809	2	B84634	probable receptor-	382	118.5	3.8	677	2	E70722	hypothetical prote
310	122.5	3.9	845	2	T12537	hypothetical prote	383	118.5	3.8	751	2	AC2098	hypothetical prote
311	122.5	3.9	1016	2	T30553	disease resistance	384	118.5	3.8	869	2	A71400	probable disease r
312	122.5	3.9	2944	2	A54949	collagen alpha 1(V	385	118.5	3.8	883	2	S57653	brevican precursor
313	122	3.9	298	2	JC4130	osteoglycin precu	386	118.5	3.8	988	2	T45717	receptor-kinase li
314	122	3.9	326	2	T24722	hypothetical prote	387	118.5	3.8	1173	2	T25893	hypothetical prote
315	122	3.9	596	2	AE1515	internalin like pr	388	118.5	3.8	1356	2	A45445	janusin precursor,
316	122	3.9	623	2	T19876	hypothetical prote	389	118.5	3.8	1607	2	T02837	long chain fatty a
317	122	3.9	672	2	B84782	probable receptor-	390	118	3.8	294	2	A37232	mucin, tracheal (A
318	122	3.9	715	2	G86239	protein F20B24.6 l	391	118	3.8	599	2	T10798	phosphorin-S - Vo
319	122	3.9	719	2	T47727	hypothetical prote	392	118	3.8	667	2	S74254	homeotic protein s
320	122	3.9	921	2	B86234	hypothetical prote	393	118	3.8	823	2	AD1935	general secretion
321	122	3.9	992	2	T05335	hypothetical prote	394	118	3.8	1134	1	ADN0711	protein-tyrosine k

395	118	2471	2	A49128	cell-fate determin	468	114	3.6	378	2	S00842	leukosialin precu
396	117.5	473	2	D85041	hypothetical prote	469	114	3.6	413	1	A34888	transcription fact
397	117.5	624	2	A55576	collagen alpha 2(X	470	114	3.6	555	1	S20100	mullerian inhibiti
398	117.5	660	2	JW0067	chitinase (EC 3.2.	471	114	3.6	586	2	T29695	hypothetical prote
399	117.5	996	2	T10725	protein kinase Xa2	472	114	3.6	633	2	S62057	proline-rich prote
400	117.5	1075	2	D70568	hypothetical prote	473	114	3.6	634	2	T00388	hypothetical prote
401	117.5	1706	2	I84499	zinc finger protei	474	114	3.6	656	2	E75468	hypothetical prote
402	117	431	2	T27904	hypothetical prote	475	114	3.6	768	2	A42755	p-selectin precurs
403	117	655	1	A46688	hepatocyte growth	476	114	3.6	1290	2	T00018	period protein hom
404	117	670	2	H96707	probable receptor	477	114	3.6	2225	2	T26063	hypothetical prote
405	117	678	2	JC4242	transcription fact	478	113.5	3.6	317	2	S55316	mucin (clone PGW-2
406	117	743	2	C84633	probable disease r	479	113.5	3.6	330	2	T46256	brevican - human (
407	117	801	2	T29018	hypothetical prote	480	113.5	3.6	538	2	T01102	disease resistance
408	117	1007	2	C84668	probable receptor-	481	113.5	3.6	896	2	B43817	transforming prote
409	117	1009	2	D75399	probable penicilli	482	113.5	3.6	907	2	A86460	99.9K hypothetical
410	117	1328	2	T43060	agrin - electric r	483	113.5	3.6	938	1	Q0BE24	nuclear antigen EB
411	117	1450	2	T30273	hypothetical prote	484	113.5	3.6	1286	2	T33476	hypothetical prote
412	117	1574	2	T13954	MEGF6 protein - ra	485	113.5	3.6	1907	2	S50893	protein-tyrosine-p
413	117	2082	2	T37056	probable multi-dom	486	113.5	3.6	2911	2	T20566	hypothetical prote
414	117	2232	2	T34434	hypothetical prote	487	113	3.6	371	2	T49908	hypothetical prote
415	116.5	279	2	S53363	mucin 5AC (clone J	488	113	3.6	377	2	A48018	mucin 7 precursor
416	116.5	439	2	S51939	chitinase (EC 3.2.	489	113	3.6	382	2	E84527	hypothetical prote
417	116.5	621	2	T38467	low density lipopr	490	113	3.6	419	2	A90888	hypothetical prote
418	116.5	787	2	T27632	hypothetical prote	491	113	3.6	419	2	H85729	hypothetical prote
419	116.5	794	2	T27632	hypothetical prote	492	113	3.6	603	2	A75373	probable N-acetylm
420	116.5	828	2	A88860	protein ZC518.3 [i	493	113	3.6	979	2	A35913	regulatory factor
421	116.5	1048	2	T31425	C-terminal domain-	494	113	3.6	982	2	A53253	microtubule-associ
422	116.5	1446	1	A45344	immediate-early pr	495	113	3.6	1002	2	T46033	receptor protein k
423	116.5	2229	2	T16199	hypothetical prote	496	113	3.6	1025	2	T45647	receptor protein k
424	116	292	2	S24169	hypothetical prote	497	113	3.6	1069	2	T29722	nuclear antigen EB
425	116	652	2	S71753	repellent protein	498	113	3.6	1247	2	T42209	neural plakophilin
426	116	660	2	AH2348	hypothetical prote	499	113	3.6	1343	2	AF0611	cell division prot
427	116	729	2	F86308	similar to disease	500	113	3.6	2688	2	I49477	alpha-A-crytallin
428	116	771	2	T02565	disease resistance	501	113	3.6	3381	2	T42389	versican precursor
429	116	808	2	B97303	hypothetical prote	502	112.5	3.6	347	2	S10571	mucin 1 precursor
430	116	845	2	T07039	Hcr9-0 protein - t	503	112.5	3.6	581	2	G96811	unknown protein T1
431	116	907	2	A24938	hypothetical T2 pr	504	112.5	3.6	731	2	B86369	hypothetical prote
432	116	1291	2	T00019	period protein hom	505	112.5	3.6	1075	2	A57377	transcription fact
433	116	1494	2	T14355	protein-tyrosine-p	506	112.5	3.6	1237	2	AC1583	internalin protein
434	116	1840	2	T30350	Grl protein - mous	507	112.5	3.6	1680	2	T01367	hypothetical prote
435	116	2531	2	A46019	notch-1 protein -	508	112.5	3.6	2479	2	F87386	conserved hypochet
436	116	2555	2	A40043	microtubule-associ	509	112.5	3.6	4006	2	T09070	probable tenascin
437	116	2774	2	A43359	hypothetical prote	510	112	3.6	241	2	S32359	glial growth facto
438	115.5	322	2	A53715	apomucin precursor	511	112	3.6	252	2	T01787	thyrotropin recept
439	115.5	513	2	AC3061	hypothetical prote	512	112	3.6	253	1	JC1319	thyrotropin recept
440	115.5	513	2	D98225	hypothetical prote	513	112	3.6	285	2	A41826	probable pheromone
441	115.5	528	2	I47141	gastric mucin (clo	514	112	3.6	383	2	S53716	delta-like homotol
442	115.5	696	2	T42659	hypothetical prote	515	112	3.6	413	2	S48756	transcription fact
443	115.5	805	2	T49385	hypothetical prote	516	112	3.6	704	2	AE2107	serine/threonine k
444	115.5	946	2	S27921	nuclear antigen EB	517	112	3.6	731	2	T04455	hypothetical prote
445	115.5	1093	2	I38633	AP17 protein - hum	518	112	3.6	742	2	F84643	hypothetical prote
446	115.5	1268	2	S52781	neurocan - mouse	519	112	3.6	764	1	QRHURH	thyrotropin recept
447	115.5	1460	1	EDBE1F	immediate-early pr	520	112	3.6	883	2	S49126	brevican precursor
448	115.5	2214	2	T16305	hypothetical prote	521	112	3.6	960	2	G84652	probable receptor-
449	115.5	3421	1	WZBBB6	367K tegument prot	522	112	3.6	990	2	T03784	probable receptor
450	115	404	2	T08549	hypothetical prote	523	112	3.6	1032	2	T34433	hypothetical prote
451	115	451	2	S74728	hypothetical prote	524	112	3.6	1289	2	D82217	hypothetical prote
452	115	461	2	T10741	extensin-like prot	525	111.5	3.6	224	2	D72861	ACOrf_91 protein -
453	115	479	1	S22542	transcription fact	526	111.5	3.6	383	2	S32975	gene BCRF2 protein
454	115	539	2	AH1216	internalin, probab	527	111.5	3.6	478	1	I47154	transcription fact
455	115	766	2	T01817	hypothetical prote	528	111.5	3.6	645	2	T05251	probable disease r
456	115	838	2	T08423	Axin homolog Ax11	529	111.5	3.6	649	2	T46500	hypothetical prote
457	115	980	2	T05414	protein kinase hom	530	111.5	3.6	1047	2	A55617	masquerade precurs
458	115	1133	2	E86308	hypothetical prote	531	111.5	3.6	1253	2	T45787	disease resistance
459	115	1220	2	A39086	Jagged protein pre	532	111.5	3.6	1298	1	EDBE75	immediate-early pr
460	115	2415	1	A59066	aggreacan precursor	533	111.5	3.6	1353	1	JH0675	restriccin precurs
461	114.5	328	2	TJ0985	hydroxyproline-ric	534	111.5	3.6	2649	2	T51023	hypothetical prote
462	114.5	409	2	T11743	pP47 protein - pig	535	111	3.5	274	2	JC8063	heart-restricted 1
463	114.5	505	2	AC1469	internalin-like pr	536	111	3.5	478	2	H86459	hypothetical prote
464	114.5	606	2	T51880	hypothetical prote	537	111	3.5	509	2	T05260	probable disease r
465	114.5	627	2	T27123	hypothetical prote	538	111	3.5	518	2	S50465	PAC2 protein - yea
466	114.5	638	2	T05606	protein kinase hom	539	111	3.5	548	2	E70546	hypothetical prote
467	114	218	2	T01104	disease resistance	540	111	3.5	603	2	S28941	coagulation factor

541	111	3.5	610	2	S35049	mucin JER57 - huma	614	109	3.5	2809	2	T30213	G-cadherin - sea u
542	111	3.5	620	2	T50150	yeast nrldi-like pr	615	108.5	3.5	308	2	JC7125	epidermal growth f
543	111	3.5	699	1	QRHU01	lutropin-choriogon	616	108.5	3.5	389	2	S27200	proline-rich prote
544	111	3.5	853	2	T17431	disease resistance	617	108.5	3.5	402	2	A84581	probable disease r
545	111	3.5	932	2	T21368	hypothetical prote	618	108.5	3.5	418	2	T15142	hypothetical prote
546	111	3.5	984	2	T48216	hypothetical prote	619	108.5	3.5	499	2	A11107	internalin E limpo
547	111	3.5	1721	1	I38902	retinoblastoma bin	620	108.5	3.5	514	2	T70699	probable ppp prote
548	111	3.5	2524	2	A35844	notch protein - Af	621	108.5	3.5	548	1	I37577	islet cell antigen
549	110.5	3.5	359	2	C50066	tyrosine decarboxy	622	108.5	3.5	662	2	A45155	mucin FIM-C.1 - Af
550	110.5	3.5	421	2	A60058	neural cell adhesi	623	108.5	3.5	698	2	I39713	cellB protein - Agr
551	110.5	3.5	512	2	G86459	Hypothetical 55.6	624	108.5	3.5	710	1	QB8E22	membrane antigen g
552	110.5	3.5	525	1	A58674	neurotrophin-3 rec	625	108.5	3.5	740	2	B84741	hypothetical prote
553	110.5	3.5	533	2	T07970	aromatic-L-amino-a	626	108.5	3.5	756	2	G86308	Similar to disease
554	110.5	3.5	565	2	JE0338	Frizzled-2 protein	627	108.5	3.5	764	2	A35956	thyrotropin recept
555	110.5	3.5	684	2	T01267	leucine-rich repea	628	108.5	3.5	783	1	A38637	Ras interactor RIN
556	110.5	3.5	803	1	S35695	neurotrophin-3 rec	629	108.5	3.5	825	1	A40026	neurotrophin-3 rec
557	110.5	3.5	815	2	B56708	extracellular sign	630	108.5	3.5	855	2	C82983	hypothetical prote
558	110.5	3.5	855	2	T07015	Cf-4A protein - to	631	108.5	3.5	1011	2	C84524	probable disease r
559	110.5	3.5	872	2	S33015	hypothetical prote	632	108.5	3.5	1125	2	B41206	microtubule-associ
560	110.5	3.5	992	2	A31666	hypothetical prote	633	108.5	3.5	1176	2	T49482	hypothetical prote
561	110.5	3.5	1207	2	A03378	KIAA0641 protein -	634	108.5	3.5	1184	2	G01763	atrophin-1 - human
562	110.5	3.5	1295	2	A32901	glp1 protein precu	635	108.5	3.5	1344	1	A35175	mucin 1 precursor,
563	110.5	3.5	1344	2	T14316	rig-1 protein - mo	636	108.5	3.5	1357	2	T29265	hypothetical prote
564	110.5	3.5	1346	2	T17412	polyketide synthas	637	108.5	3.5	1487	2	T02850	heparan sulfate pr
565	110.5	3.5	1736	2	T00391	hypothetical prote	638	108.5	3.5	3707	2	S18252	hypothetical 35.5X
566	110.5	3.5	2476	2	T34022	zonadhesin - pig	639	108	3.4	348	2	JQ0431	flagellar hook-len
567	110	3.5	275	2	T51437	hypothetical prote	640	108	3.4	409	2	AG0752	glycoprotein C - h
568	110	3.5	391	2	T04609	hypothetical prote	641	108	3.4	511	1	VGBE1K	chitinase (EC 3.2.
569	110	3.5	549	2	S32987	hypothetical prote	642	108	3.4	542	2	I39540	proline-rich prote
570	110	3.5	691	2	D84889	probable receptor-	643	108	3.4	544	2	T17547	probable serine/th
571	110	3.5	708	2	D96711	hypothetical prote	644	108	3.4	550	2	T36746	dihydrolipoamide S
572	110	3.5	719	2	T02154	protein kinase hom	645	108	3.4	638	1	XXAV	probable disease r
573	110	3.5	764	2	I48882	thyrotropin recept	646	108	3.4	862	2	S43922	versican - pig-tai
574	110	3.5	846	2	H70599	hypothetical prote	647	108	3.4	996	2	JE0237	apolipoprotein E r
575	110	3.5	846	2	T21700	hypothetical prote	648	108	3.4	1017	2	T31354	probable potassium
576	110	3.5	951	2	A96770	hypothetical prote	649	108	3.4	1217	2	T51140	disease resistance
577	110	3.5	1123	2	D96756	receptor-like prot	650	108	3.4	1217	2	T51140	disease resistance
578	110	3.5	1483	2	E86143	F6F3.12 protein -	651	108	3.4	1217	2	T51141	alpha-fetoprotein
579	110	3.5	1711	1	A55148	protein-tyrosine-p	652	108	3.4	2783	1	A41948	unconventional myo
580	110	3.5	2703	1	A24420	notch protein - fr	653	108	3.4	3511	2	A59295	polyketide synthas
581	110	3.5	2715	2	T13049	eyelid - fruit fly	654	108	3.4	4613	2	T17409	PK506 polyketide s
582	110	3.5	3942	2	T42730	Bassoon protein -	655	108	3.4	7576	2	T17428	hypothetical prote
583	109.5	3.5	213	2	A86228	hypothetical prote	656	107.5	3.4	363	2	H87702	hypothetical prote
584	109.5	3.5	279	2	T10361	hypothetical prote	657	107.5	3.4	369	2	S20500	hydroxyproline-ric
585	109.5	3.5	318	2	T29479	hypothetical prote	658	107.5	3.4	414	2	C96770	hypothetical prote
586	109.5	3.5	428	2	E71415	probable coll wall	659	107.5	3.4	427	2	S74211	PAS-6/7 protein pr
587	109.5	3.5	473	2	S36553	L2 protein - human	660	107.5	3.4	536	2	H71563	hypothetical prote
588	109.5	3.5	507	2	T44768	antifreeze glycope	661	107.5	3.4	604	2	S25203	smR protein - Str
589	109.5	3.5	538	2	S57459	hook-containing pr	662	107.5	3.4	655	2	G96524	protein TNF5.9 [i
590	109.5	3.5	558	2	JC5878	plasma hyaluronan-	663	107.5	3.4	832	2	A31246	neurogenic protein
591	109.5	3.5	593	1	S22544	transcription fact	664	107.5	3.4	880	2	S00670	neurogenic repetit
592	109.5	3.5	612	2	I73633	gene trkC protein	665	107.5	3.4	881	2	B98320	cellulose synthase
593	109.5	3.5	825	2	A55178	neurotrophin recep	666	107.5	3.4	1009	2	T45645	receptor kinase-li
594	109.5	3.5	839	1	I73632	neurotrophin-3 rec	667	107.5	3.4	1099	2	A56155	tumor suppressor p
595	109.5	3.5	874	2	E97302	hypothetical prote	668	107.5	3.4	1206	2	S24407	formin isoform IV
596	109.5	3.5	878	2	T21621	hypothetical prote	669	107.5	3.4	1324	2	S28863	DNA-binding protei
597	109.5	3.5	954	2	T17965	hypothetical prote	670	107.5	3.4	1468	2	S11515	formin - mouse
598	109.5	3.5	1299	2	T47182	hypothetical prote	671	107.5	3.4	3534	2	T42567	segment protein 2
599	109.5	3.5	1776	1	RRWPM	genome polyprotein	672	107	3.4	176	1	A46606	platelet glycoprot
600	109.5	3.5	2531	2	T31070	notch homolog - se	673	107	3.4	228	2	S53504	extensin-like prot
601	109.5	3.5	2717	2	A34203	DNA-binding protei	674	107	3.4	273	2	A28512	fibronectin - chic
602	109	3.5	379	2	T05441	proline-rich prote	675	107	3.4	354	2	A48931	transmembrane glyc
603	109	3.5	379	2	D85257	extensin-like prot	676	107	3.4	358	1	WMBE38	infected cell prot
604	109	3.5	395	2	I52842	CD43 Lp-3 antigen	677	107	3.4	416	1	SKXLAG	dermal gland prote
605	109	3.5	395	2	A43545	leukostialin CD43 p	678	107	3.4	447	2	A39321	mucin - rat (fragm
606	109	3.5	403	2	S52796	prip2 protein - hu	679	107	3.4	452	2	C41602	transcription fact
607	109	3.5	436	2	JQ1696	pistil extensin-li	680	107	3.4	518	1	KFHU12	hypothetical prote
608	109	3.5	431	2	T04868	hypothetical prote	681	107	3.4	615	1	KFHU12	coagulation factor
609	109	3.5	437	2	A54595	transcription fact	682	107	3.4	650	2	S59630	disaccharide alpha
610	109	3.5	538	2	C96756	receptor-like prot	683	107	3.4	840	1	S69204	pheromone response
611	109	3.5	613	2	T42671	hypothetical prote	684	107	3.4	915	2	T12526	hypothetical prote
612	109	3.5	833	2	S19087	gene Delta protein	685	107	3.4	1063	1	GNWVR4	structural polypro
613	109	3.5	1611	2	T38236	hypothetical prote	686	107	3.4	1376	2	G00043	osteonidogen - hum

687	107	3.4	1389	2	I58157	periaxin - rat	760	105	3.3	1133	2	A54164	sterol regulatory
688	107	3.4	2723	2	T03221	probable polyketid	761	105	3.3	1135	2	T30561	scythe protein - A
689	107	3.4	7463	2	T36248	CDA peptide synthe	762	105	3.3	1136	1	S57845	protein-tyrosine k
690	106.5	3.4	304	2	A32993	transcription fact	763	105	3.3	1456	2	T01397	LTR gag/pol polypr
691	106.5	3.4	353	2	A41558	N-syndecan - rat (764	105	3.3	1858	2	D75489	hypothetical prote
692	106.5	3.4	505	2	B46629	mucin 6, gastric (765	105	3.3	1844	2	S01956	hypothetical prote
693	106.5	3.4	509	2	D86911	conserved hypoteth	766	105	3.3	2133	2	T30637	hypothetical prote
694	106.5	3.4	509	2	T10013	probable phosphopr	767	105	3.3	2409	1	A60979	versican precursor
695	106.5	3.4	517	2	AD1570	internalin, probab	768	105	3.3	2769	1	UIBO	thryoglobulin prec
696	106.5	3.4	620	2	S06733	hydroxyproline-ric	769	104.5	3.3	329	2	T17033	leucine rich repea
697	106.5	3.4	827	2	AC2963	ce1B protein (impo	770	104.5	3.3	407	2	C70816	hypothetical prote
698	106.5	3.4	925	2	H96638	protein Tf9.20 [i	771	104.5	3.3	464	2	T35943	probable hydrolyti
699	106.5	3.4	998	2	C75489	conserved hypoteth	772	104.5	3.3	530	2	T32812	hypothetical prote
700	106.5	3.4	1003	2	T13856	ker protein - frui	773	104.5	3.3	639	2	G02919	transcription fact
701	106.5	3.4	1161	2	S57180	probable membrane	774	104.5	3.3	662	2	T04856	hypothetical prote
702	106.5	3.4	1184	2	S50832	atrophin-1 - human	775	104.5	3.3	700	2	A42395	lutropin receptor
703	106.5	3.4	1305	2	AB0168	probable cell divi	776	104.5	3.3	707	1	A34458	gelatinase B (EC 3
704	106.5	3.4	1442	2	T42607	transcription acti	777	104.5	3.3	707	1	A53796	gelatinase B (EC 3
705	106.5	3.4	1892	2	T18314	hypothetical prote	778	104.5	3.3	744	2	T35192	probable ABC trans
706	106.5	3.4	2090	2	S26058	probable transform	779	104.5	3.3	755	2	T20950	hypothetical prote
707	106.5	3.4	2453	2	S60254	nuclear receptor c	780	104.5	3.3	909	1	QRXLL1	LDL receptor 1 pre
708	106	3.4	135	2	T49396	AtAGP4 - Arabidops	781	104.5	3.3	960	1	S28262	kinesin-related pr
709	106	3.4	167	2	A33532	mucin SMUC-40 - hu	782	104.5	3.3	1117	2	JC4934	delta-crystallin/E
710	106	3.4	216	2	I51920	mucin - rheus mac	783	104.5	3.3	1194	2	E96624	hypothetical prote
711	106	3.4	287	2	S65765	chitinase (EC 3.2.	784	104.5	3.3	1241	2	T37190	chitinase B (EC 3
712	106	3.4	405	2	S78691	flagellar hook-len	785	104.5	3.3	1505	2	JC4851	hypothetical prote
713	106	3.4	431	2	S47538	acrosin (EC 3.4.21	786	104.5	3.3	1851	2	T19964	lymphotoxin-beta -
714	106	3.4	435	2	D41802	transcription fact	787	104.5	3.3	1898	2	S46216	leukocyte antigen-
715	106	3.4	443	2	B39794	transcription fact	788	104.5	3.3	2117	2	T36180	CDA peptide synthe
716	106	3.4	449	2	A24993	cellulase (EC 3.2.	789	104	3.3	232	2	A60095	larval glue protei
717	106	3.4	567	2	A5977	Rab geranylgeranyl	790	104	3.3	306	2	I49139	hypothetical prote
718	106	3.4	666	2	B70803	hypothetical prote	791	104	3.3	318	2	B64900	hypothetical prote
719	106	3.4	701	2	D48613	cag polypeptide -	792	104	3.3	326	2	A46676	CD68 homolog macro
720	106	3.4	818	2	T01105	disease resistance	793	104	3.3	332	2	S43988	protein phosphatas
721	106	3.4	822	2	T51049	related to nucleol	794	104	3.3	360	2	S68209	sd22 protein homo
722	106	3.4	850	2	S56012	gastric mucin MUC5	795	104	3.3	365	2	A39481	serum response fac
723	106	3.4	901	2	A49227	siadase - Actino	796	104	3.3	426	2	D88103	protein W10G11.6 l
724	106	3.4	914	2	T17233	hypothetical prote	797	104	3.3	440	2	I49681	glycerolaldehyde-3-p
725	106	3.4	1064	2	A40136	fibropellin Ia - s	798	104	3.3	470	2	S36536	L2 protein - human
726	106	3.4	1603	2	A48613	gag/pol polypeptei	799	104	3.3	537	2	A46611	myosin-binding pro
727	106	3.4	1958	2	B40505	hypothetical prote	800	104	3.3	538	2	S65764	chitinase (EC 3.2.
728	106	3.4	2554	1	TVF77L	kinase-related pro	801	104	3.3	593	2	S49525	glycoprotein G - s
729	106	3.4	3938	2	T42761	Bassoon protein -	802	104	3.3	712	1	I46031	gelatinase B (EC 3
730	105.5	3.4	395	2	T01392	leucine-rich repea	803	104	3.3	895	2	S20582	dystrophin-associa
731	105.5	3.4	486	2	A41537	DNA-binding protei	804	104	3.3	927	2	T24031	hypothetical prote
732	105.5	3.4	510	2	A42750	insulinoma-associa	805	104	3.3	1045	2	T16275	hypothetical prote
733	105.5	3.4	668	2	T05257	probable disease r	806	104	3.3	1547	2	T28657	blackjack protein,
734	105.5	3.4	688	2	T04568	protein kinase hom	807	104	3.3	1575	2	S68448	synaptotagmin, 170K
735	105.5	3.4	695	2	S62400	amphiphysin (clone	808	104	3.3	1711	2	T31337	1,4-beta-glucanase
736	105.5	3.4	772	2	T13078	KIAA0992 protein -	809	104	3.3	1744	2	A54970	tensin, cardiac mu
737	105.5	3.4	780	2	A48143	HP-1 regulatory el	810	104	3.3	3507	2	T34513	hypothetical prote
738	105.5	3.4	952	2	S32954	hypothetical prote	811	103.5	3.3	206	1	NBHUIB	platelet glycoprot
739	105.5	3.4	1132	2	A35098	MHC class III hist	812	103.5	3.3	264	2	PQ0478	pistil extensin-li
740	105.5	3.4	1172	2	T00065	hypothetical prote	813	103.5	3.3	281	2	D70845	hypothetical prote
741	105.5	3.4	1621	2	T15264	hypothetical prote	814	103.5	3.3	393	2	PQ0479	pistil extensin-li
742	105.5	3.4	1712	2	A38261	masking protein pr	815	103.5	3.3	411	1	I55604	platelet glycoprot
743	105.5	3.4	1839	1	RRWPEM	genome polypeptei	816	103.5	3.3	419	2	T49292	hypothetical prote
744	105.5	3.4	2477	2	T14428	fibronectin precur	817	103.5	3.3	444	1	A39794	transcription fact
745	105.5	3.4	3033	1	JQ1303	genome polypeptei	818	103.5	3.3	489	2	F75591	p49 secreted prote
746	105	3.3	349	2	T05857	hypothetical prote	819	103.5	3.3	625	2	A26456	nicotinic acetylch
747	105	3.3	422	2	T37891	interleukin-11 rec	820	103.5	3.3	654	2	T33044	hypothetical prote
748	105	3.3	454	2	E75291	probable cell wall	821	103.5	3.3	889	2	F96637	hypothetical prote
749	105	3.3	460	2	T33110	hypothetical prote	822	103.5	3.3	899	2	T20123	hypothetical prote
750	105	3.3	486	1	A57601	transcription fact	823	103.5	3.3	958	2	T00353	hypothetical prote
751	105	3.3	511	1	VGBEF4	glycoprotein C - h	824	103.5	3.3	975	2	I48974	receptor-protein t
752	105	3.3	566	2	T34842	probable transfera	825	103.5	3.3	980	2	S54986	regulatory protein
753	105	3.3	620	2	A70525	hypothetical prote	826	103.5	3.3	1020	2	A29355	fibronectin - chic
754	105	3.3	658	2	T08153	cysteine proteinas	827	103.5	3.3	1144	2	A54810	TMV resistance pro
755	105	3.3	730	2	JC1456	gelatinase B (EC 3	828	103.5	3.3	1171	2	T35548	hypothetical prote
756	105	3.3	764	2	JC5643	thyroid stimulatn	829	103.5	3.3	1268	2	T31420	C-terminal domain-
757	105	3.3	847	1	UC3800	mixed-lineage prot	830	103.5	3.3	1590	2	B86398	protein T7N9.24 [i
758	105	3.3	895	2	I54343	dysglycan - hum	831	103.5	3.3	1603	2	S23810	collagen alpha 1(X
759	105	3.3	976	2	A36355	protein-tyrosine k	832	103.5	3.3	1638	2	A42091	transcription acti

833	103.5	3.3	1733	1	B45344	probable nuclear a	906	102	3.3	567	2	JC5538	Rab geranylgeranyl
834	103.5	3.3	3729	2	T17410	polyketide synthas	907	102	3.3	585	1	B70747	probable serine/th
835	103	3.3	168	2	S52994	arabinogalactan-li	908	102	3.3	650	2	B87791	protein B0207.1 [i
836	103	3.3	231	2	T87905	hypothetical prote	909	102	3.3	670	2	S22293	zinc finger protei
837	103	3.3	227	2	T27905	hypothetical prote	910	102	3.3	715	2	T12534	hypothetical prote
838	103	3.3	263	2	S01360	salivary glue prot	911	102	3.3	722	2	I48324	DELTA-like 1 - mou
839	103	3.3	362	2	A44083	meq protein - Mare	912	102	3.3	728	2	D86278	hypothetical prote
840	103	3.3	367	2	AC1328	internalin protein	913	102	3.3	890	2	E84846	probable receptor-
841	103	3.3	379	2	T16213	APX-1 protein homo	914	102	3.3	896	1	A35782	cytokine receptor
842	103	3.3	394	2	C84905	probable extensin	915	102	3.3	923	2	A39596	progesterone recep
843	103	3.3	515	2	F70904	hypothetical prote	916	102	3.3	963	2	A55926	DNA binding protei
844	103	3.3	535	1	S76953	protein kinase (EC	917	102	3.3	1008	2	T04462	hypothetical prote
845	103	3.3	550	2	G70597	probable proteinase	918	102	3.3	1021	2	H75423	hypothetical prote
846	103	3.3	575	2	JG0181	X11L2 protein - hu	919	102	3.3	1032	2	D83637	serine/threonine p
847	103	3.3	611	2	G68387	unknown protein [i	920	102	3.3	1052	2	B49120	protein-tyrosine k
848	103	3.3	648	2	T35120	hypothetical prote	921	102	3.3	1069	2	D85383	hypothetical prote
849	103	3.3	701	2	F48613	gag polyprotein -	922	102	3.3	1137	2	A86335	T20H2.9 protein -
850	103	3.3	793	2	JC7390	thyroid stimulat	923	102	3.3	1166	2	T13958	synGAP-b1 protein
851	103	3.3	799	1	TVRTTB	nerve growth facto	924	102	3.3	1249	2	T14270	Ras-GTPase activat
852	103	3.3	813	2	T04313	protein kinase Xa2	925	102	3.3	1293	2	T14259	ras GTPase-activat
853	103	3.3	851	2	S67285	NDP1 protein - yea	926	102	3.3	1692	2	A39988	adenylate cyclase
854	103	3.3	863	2	A55173	cf-9 protein precu	927	102	3.3	1895	2	S19151	hypothetical prote
855	103	3.3	915	2	S36327	clathrin assembly	928	102	3.3	2218	2	B84683	hypothetical prote
856	103	3.3	1040	2	T29092	TSC-22 protein hom	929	102	3.3	2437	2	S42612	transmembrane prot
857	103	3.3	1121	2	A82809	exodeoxyribonuclea	930	102	3.3	2440	2	S39162	transcription coac
858	103	3.3	1199	2	A40670	nuclear envelope p	931	102	3.3	2441	2	S39161	CREB-binding prote
859	103	3.3	1201	2	G86441	unknown protein [i	932	102	3.3	3124	2	A40020	collagen alpha 1(X
860	103	3.3	1275	2	T33369	hypothetical prote	933	102	3.3	5147	1	IJFFTM	cadherin-related c
861	103	3.3	1340	2	A39808	proteoglycan core	934	101.5	3.2	98	2	S53367	mucin SAC (clone M
862	103	3.3	1541	2	T02831	AAA protein L4171.	935	101.5	3.2	173	2	T47176	hypothetical prote
863	103	3.3	1894	2	C54689	protein-tyrosine-p	936	101.5	3.2	244	2	A40428	non-specific cross-
864	103	3.3	2207	1	GNNY5P	genome polyprotein	937	101.5	3.2	372	2	T29359	hypothetical prote
865	103	3.3	2481	2	A43908	fibronectin - Afri	938	101.5	3.2	409	2	T43599	yop targeted effec
866	103	3.3	3133	2	S52093	hemocytin - silkw	939	101.5	3.2	547	2	B56573	nuclear pore compl
867	102.5	3.3	217	2	S01358	salivary glue prot	940	101.5	3.2	654	2	C87587	hypothetical prote
868	102.5	3.3	252	2	T04739	hypothetical prote	941	101.5	3.2	657	2	B84869	probable SPI6 prot
869	102.5	3.3	316	2	T31880	hypothetical prote	942	101.5	3.2	710	2	T44753	hypothetical prote
870	102.5	3.3	338	2	I53043	transforming prote	943	101.5	3.2	733	2	A87168	C-Delta-1 - chicke
871	102.5	3.3	352	2	S17313	transcription fact	944	101.5	3.2	833	2	AF2089	conserved hypotet
872	102.5	3.3	371	2	F70555	hypothetical prote	945	101.5	3.2	869	2	A55384	hypothetical prote
873	102.5	3.3	379	2	S31719	proline-rich prote	946	101.5	3.2	869	2	A55384	transcription fact
874	102.5	3.3	383	2	B86272	protein F16A14.12	947	101.5	3.2	921	2	S40495	collagen alpha 1(I
875	102.5	3.3	385	2	S53718	homeotic protein d	948	101.5	3.2	947	2	G86420	probable receptor-
876	102.5	3.3	385	2	A54785	preadipocyte facto	949	101.5	3.2	977	2	I52657	seizure-related pr
877	102.5	3.3	421	2	T32709	core protein homol	950	101.5	3.2	984	1	A34076	protein-tyrosine k
878	102.5	3.3	507	1	A32385	erythropoietin rec	951	101.5	3.2	1034	2	JC5569	serine proteinase
879	102.5	3.3	627	2	D75393	serine proteinase,	952	101.5	3.2	1039	2	A85096	hypothetical prote
880	102.5	3.3	674	2	T05264	probable serine/th	953	101.5	3.2	1429	2	S06434	homeotic protein 1
881	102.5	3.3	706	2	E30411	synapsin Ia - bovi	954	101.5	3.2	1668	2	T13748	sex comb protein -
882	102.5	3.3	730	1	I52580	gelatinase B (EC 3	955	101.5	3.2	1733	2	S27939	tensin - chicken
883	102.5	3.3	760	1	S07896	transcription fact	956	101.5	3.2	4543	1	A53102	alpha-2-macroglobu
884	102.5	3.3	904	2	T46170	disease resistance	957	101	3.2	240	2	B24264	proline-rich prote
885	102.5	3.3	907	2	E96636	hypothetical prote	958	101	3.2	249	2	S72619	hypothetical prote
886	102.5	3.3	942	1	JQ1574	protein kinase TWK	959	101	3.2	294	2	T34537	hypothetical prote
887	102.5	3.3	964	2	JC5545	integrin beta-4 pr	960	101	3.2	360	2	S25561	transcription fact
888	102.5	3.3	1013	2	T46422	hypothetical prote	961	101	3.2	373	2	A44478	probable cell grow
889	102.5	3.3	1115	1	IJMSNL	neural cell adhesi	962	101	3.2	401	2	A48423	engrailed homeod
890	102.5	3.3	1223	1	T31316	hypothetical prote	963	101	3.2	482	2	A44997	merozoite surfaco
891	102.5	3.3	1350	2	G36793	hypothetical prote	964	101	3.2	492	2	B85911	probable penicilli
892	102.5	3.3	1367	1	S48478	glucan 1,4-alpha-g	965	101	3.2	574	2	B87619	sensor histidine k
893	102.5	3.3	1678	2	T35447	hypothetical prote	966	101	3.2	610	2	A28798	myosin-light-chain
894	102.5	3.3	1779	2	T31085	xylanase - Caldice	967	101	3.2	613	2	A40497	diacylglycerol S
895	102.5	3.3	1813	2	T30564	resistance protein	968	101	3.2	615	1	XXHU	dihydroliipoamide S
896	102.5	3.3	1863	2	S46217	protein-tyrosine-p	969	101	3.2	628	2	JQ0110	hypothetical 69K p
897	102.5	3.3	1875	2	A36429	integrin beta-4 ch	970	101	3.2	671	2	D84648	probable disease r
898	102.5	3.3	2207	2	S09553	genome polyprotein	971	101	3.2	688	2	T18263	S-layer protein -
899	102	3.3	301	2	JQ1663	hybrid proline-ric	972	101	3.2	700	2	D70951	probable UvrD - My
900	102	3.3	307	2	S36779	ribosome-binding p	973	101	3.2	739	2	I56187	transcription fact
901	102	3.3	317	2	A28996	proline-rich prote	974	101	3.2	796	2	T21460	hypothetical prote
902	102	3.3	353	2	B36963	bcsA 5'-region pro	975	101	3.2	846	1	Q0BEC3	HQR1 protein - hu
903	102	3.3	413	2	T49545	hypothetical prote	976	101	3.2	1043	2	A56037	DNA-binding protei
904	102	3.3	532	2	S74453	hypothetical prote	977	101	3.2	1127	2	T32404	hypothetical prote
905	102	3.3	554	1	FQHUMP	macrophage colony-	978	101	3.2	1257	2	S28764	neurocan precursor

979	101	3.2	1367	2	T33819	hypothetical prote	1052	99.5	3.2	352	2	S05500	Ig alpha-1 chain C
980	101	3.2	1513	2	A54895	mucin 2, chicken	1053	99.5	3.2	353	1	AlHU	Ig alpha-1 chain C
981	101	3.2	1792	2	A57075	tensin - chicken	1054	99.5	3.2	353	3	S36438	EpPT protein - hyd
982	101	3.2	2946	2	T15840	hypothetical prote	1055	99.5	3.2	375	1	TGHUM4	monocyte surface g
983	101	3.2	3176	2	CGHJ3A	collagen alpha 3(V	1056	99.5	3.2	383	1	VGHEKG	glycoprotein precu
984	100.5	3.2	138	2	D96715	protein F4N2.10 [i	1057	99.5	3.2	387	2	B49175	Notch A protein -
985	100.5	3.2	262	2	T33408	hypothetical prote	1058	99.5	3.2	392	2	B48423	homeotic protein e
986	100.5	3.2	262	2	E88400	protein H34I24.2 [1059	99.5	3.2	393	1	VGSED2	glycoprotein D - h
987	100.5	3.2	269	2	T26957	hypothetical prote	1060	99.5	3.2	420	2	T46910	hypothetical prote
988	100.5	3.2	274	2	T46041	hypothetical prote	1061	99.5	3.2	420	2	JC4199	heat-shock protein
989	100.5	3.2	283	2	E88597	protein Y47D3B.6 [1062	99.5	3.2	476	1	C70986	probable serine/th
990	100.5	3.2	314	2	T48514	hypothetical prote	1063	99.5	3.2	491	2	F70699	probable pppA prot
991	100.5	3.2	384	2	T50921	carbamoyl-phosphat	1064	99.5	3.2	530	2	S52215	hypothetical prote
992	100.5	3.2	401	2	S65138	glycoprotein antig	1065	99.5	3.2	539	2	T28770	hypothetical prote
993	100.5	3.2	440	2	JC7807	Wiskott-Aldrich sy	1066	99.5	3.2	647	2	T43952	hypothetical prote
994	100.5	3.2	504	2	AG2373	hypothetical prote	1067	99.5	3.2	665	2	S62328	kinesin-like DNA b
995	100.5	3.2	504	2	S56745	mucin (clone pW31	1068	99.5	3.2	702	2	A86383	76.4K protein kina
996	100.5	3.2	512	2	E59437	F02569_2 protein [1069	99.5	3.2	802	2	T24293	hypothetical prote
997	100.5	3.2	597	2	TQ0107	hypothetical 66K p	1070	99.5	3.2	851	2	AD1427	internalin, probab
998	100.5	3.2	677	2	T39713	zinc finger protei	1071	99.5	3.2	853	1	IJBONC	neural cell adhesi
999	100.5	3.2	798	2	T43248	hypothetical prote	1072	99.5	3.2	886	2	T35469	probable ATP /GTP-
1000	100.5	3.2	906	2	A43817	transforming prote	1073	99.5	3.2	903	2	T19209	probable protein k
1001	100.5	3.2	975	2	S33121	homeotic protein C	1074	99.5	3.2	949	2	T24294	hypothetical prote
1002	100.5	3.2	1024	2	T27631	hypothetical prote	1075	99.5	3.2	958	2	E82994	glycine cleavage s
1003	100.5	3.2	1030	2	H88859	protein ZC518.2 [i	1076	99.5	3.2	961	1	TSHUP4	thrombospondin 4 p
1004	100.5	3.2	1106	1	TVHUGL	transforming prote	1077	99.5	3.2	1013	2	T33470	hypothetical prote
1005	100.5	3.2	1131	2	F96662	hypothetical prote	1078	99.5	3.2	1016	2	T41720	hypothetical prote
1006	100.5	3.2	1138	1	S24066	protein-tyrosine k	1079	99.5	3.2	1056	2	A53767	mucin MUC5B, trach
1007	100.5	3.2	1220	2	T48928	disease resistance	1080	99.5	3.2	1122	2	T47424	hypothetical prote
1008	100.5	3.2	1273	2	S58782	SEC31 protein - ye	1081	99.5	3.2	1220	2	T06403	resistance complex
1009	100.5	3.2	1323	2	T42653	spalt protein - mo	1082	99.5	3.2	1390	2	T31353	polypeptide - Arab
1010	100.5	3.2	2327	2	T20230	aggreca - bovine	1083	99.5	3.2	1473	2	T31422	C-terminal domain-
1011	100.5	3.2	2562	2	T14266	Xin protein - chic	1084	99.5	3.2	1742	2	T17120	cellulase (EC 3.2.
1012	100.5	3.2	3562	2	A47171	chondroitin sulfat	1085	99.5	3.2	3869	2	A48205	All-1 protein +GTE
1013	100.5	3.2	4548	1	S00657	apoptoteint(a) (EC	1086	99	3.2	134	2	PQ0476	pistil extensin-li
1014	100	3.2	230	2	A56210	neu differentiatio	1087	99	3.2	214	2	T09854	proline-rich cell
1015	100	3.2	311	2	B86211	hypothetical prote	1088	99	3.2	307	1	GSFF3	salivary glue prot
1016	100	3.2	334	2	G02409	protein kinase C-b	1089	99	3.2	329	2	B41344	lutropin-choriogon
1017	100	3.2	366	2	S61796	T-cell-specific tr	1090	99	3.2	329	2	D41344	lutropin-choriogon
1018	100	3.2	367	2	A33950	yopM protein - yer	1091	99	3.2	331	2	C41344	leucine-rich repea
1019	100	3.2	474	2	S15921	protein TPX-VT3 -	1092	99	3.2	358	2	T01296	leucine-rich repea
1020	100	3.2	476	2	C39481	serum response fac	1093	99	3.2	415	1	A34170	acrosin (EC 3.4.21
1021	100	3.2	510	2	H84824	En/Spm-like transp	1094	99	3.2	428	2	S45361	LRR47 protein - fr
1022	100	3.2	535	2	T17212	hypothetical prote	1095	99	3.2	447	2	T34992	probable lipoprote
1023	100	3.2	549	2	C87719	protein R119, 6 lim	1096	99	3.2	466	2	T06416	cysteine proteinas
1024	100	3.2	556	2	D70940	probable PPE prote	1097	99	3.2	511	2	AC0941	probable ABC trans
1025	100	3.2	562	2	S75308	DNA ligase (EC 6.5	1098	99	3.2	543	2	S25128	61K protein - Auto
1026	100	3.2	596	2	G75457	tetratricopeptide	1099	99	3.2	564	2	I53106	gene g11 protein -
1027	100	3.2	628	2	S44138	polyadenylate-bind	1100	99	3.2	569	2	F75381	probable two-compo
1028	100	3.2	673	2	AF1143	internalin protein	1101	99	3.2	616	2	C75588	conserved hypothet
1029	100	3.2	698	2	T51915	hypothetical prote	1102	99	3.2	638	2	T51383	receptor protein k
1030	100	3.2	698	2	T17261	hypothetical prote	1103	99	3.2	641	2	C84726	probable receptor-
1031	100	3.2	699	2	T09069	probable cAMP-resp	1104	99	3.2	686	2	F96542	probable protein k
1032	100	3.2	713	2	T44447	neuregulin-3 [impo	1105	99	3.2	696	2	A41344	lutropin-choriogon
1033	100	3.2	725	2	T01268	leucine-rich repea	1106	99	3.2	701	2	S61239	hypothetical prote
1034	100	3.2	756	2	C87432	hypothetical prote	1107	99	3.2	770	1	S30293	transcription fact
1035	100	3.2	776	2	A46593	neuroendocrine-spe	1108	99	3.2	814	2	JC7389	thyroid stimulat
1036	100	3.2	881	2	T01269	serine/threonine-s	1109	99	3.2	860	2	C86203	hypothetical prote
1037	100	3.2	1109	2	C84545	probable disease r	1110	99	3.2	940	2	H86420	probable receptor-
1038	100	3.2	1161	2	T45294	hypothetical prote	1111	99	3.2	963	2	T19140	hypothetical prote
1039	100	3.2	1182	2	T48378	hairless protein -	1112	99	3.2	1000	2	C82630	serine proteinase
1040	100	3.2	1240	2	T06404	resistance complex	1113	99	3.2	1097	2	T49187	hypothetical prote
1041	100	3.2	1420	2	T37781	probable cytoskele	1114	99	3.2	1147	2	T42627	ADP-ribosylation f
1042	100	3.2	1687	2	T30176	EGF repeat transme	1115	99	3.2	1217	2	T52348	disease resistance
1043	100	3.2	1791	2	T02345	hypothetical prote	1116	99	3.2	1317	2	T03748	apoptosis associat
1044	100	3.2	1802	2	T00030	bacterial blight-r	1117	99	3.2	1405	2	T04426	hypothetical prote
1045	100	3.2	1897	1	TDHULK	leukocyte antigen-	1118	99	3.2	1532	2	A61262	collagen alpha 1(X
1046	100	3.2	2459	2	AF21336	peptide synthetase	1119	99	3.2	1538	2	E70874	probable pps8 prot
1047	99.5	3.2	108	2	S08315	cell wall protein	1120	99	3.2	1694	2	S50065	sialoadhesin - mou
1048	99.5	3.2	177	2	T07642	PEARL1 protein h	1121	99	3.2	1799	1	S44920	zk688.5 protein -
1049	99.5	3.2	230	2	A44074	probable EGF-like	1122	99	3.2	2029	1	TDFFLK	protein-tyrosine-p
1050	99.5	3.2	280	2	T48713	Phox2 homeodomain	1123	99	3.2	2088	2	E71436	hypothetical prote
1051	99.5	3.2	293	2	C75421	hypothetical prote	1124	99	3.2	6420	2	T30283	polyketide synthas

1125	98.5	3.1	230	2	T22763	hypothenical prote	1198	97.5	3.1	362	2	S22395	fetuin precursor -
1126	98.5	3.1	234	2	D88560	protein F58A4.1 [l	1199	97.5	3.1	429	2	JC4965	elk1 protein - mou
1127	98.5	3.1	342	2	T77461	luteinizing hormon	1200	97.5	3.1	460	2	T23087	hypothenical prote
1128	98.5	3.1	349	2	T15422	hypothenical prote	1201	97.5	3.1	464	2	T23087	extensin - Volvox
1129	98.5	3.1	379	2	S50125	larval glue protei	1202	97.5	3.1	497	2	F83634	hypothenical prote
1130	98.5	3.1	385	2	T18180	proline-rich prote	1203	97.5	3.1	511	2	T43282	alp21 protein - fi
1131	98.5	3.1	393	2	S62335	171-7 protein - fr	1204	97.5	3.1	521	2	S54266	glycoprotein gc -
1132	98.5	3.1	434	1	A35005	u-plasminogen acti	1205	97.5	3.1	531	2	B55066	tyrosine decarboxy
1133	98.5	3.1	464	2	T26553	hypothenical prote	1206	97.5	3.1	563	2	A75594	ferredoxin-nitrite
1134	98.5	3.1	486	2	B39481	serum response fac	1207	97.5	3.1	574	1	A48501	probable protein-1
1135	98.5	3.1	514	2	A44100	cell adhesion mole	1208	97.5	3.1	587	2	T41653	probable transcrip
1136	98.5	3.1	633	2	T47346	receptor protein k	1209	97.5	3.1	614	2	T33149	hypothenical prote
1137	98.5	3.1	700	2	T77463	luteinizing hormon	1210	97.5	3.1	626	2	B70754	probable serine/th
1138	98.5	3.1	700	2	A49744	lutropin-choriogon	1211	97.5	3.1	627	1	JC6534	protein kinase 1 (
1139	98.5	3.1	707	2	A46302	PTB-associated spl	1212	97.5	3.1	627	2	AB0535	hypothenical prote
1140	98.5	3.1	770	2	T22808	hypothenical prote	1213	97.5	3.1	631	1	A36749	transcription fact
1141	98.5	3.1	803	2	F59433	RhoGAP protein [im	1214	97.5	3.1	662	2	D40228	neurexin II-beta p
1142	98.5	3.1	837	2	A42112	mucin-like peptide	1215	97.5	3.1	676	1	EDB823	immediate-early pr
1143	98.5	3.1	862	2	E88594	protein Y48A6B.11	1216	97.5	3.1	710	2	D96728	hypothenical prote
1144	98.5	3.1	885	2	B66257	NBS/LRR disease re	1217	97.5	3.1	754	2	AC2807	OmpA family protei
1145	98.5	3.1	921	2	D86293	F7H2.22 protein -	1218	97.5	3.1	754	2	B97586	hypothenical prote
1146	98.5	3.1	947	2	T26314	hypothenical prote	1219	97.5	3.1	814	2	G02390	disintegrin-like m
1147	98.5	3.1	1087	2	T31100	probable potassium	1220	97.5	3.1	817	2	S51342	verprolin - yeast
1148	98.5	3.1	1272	2	T30248	fragile X mental r	1221	97.5	3.1	830	2	T17672	chitinase-like pro
1149	98.5	3.1	1281	2	T00346	hypothenical prote	1222	97.5	3.1	893	2	H96651	protein T3P18.19 [
1150	98.5	3.1	1309	2	T00078	probable RNA-direc	1223	97.5	3.1	909	1	A54809	disease resistance
1151	98.5	3.1	1396	2	A44453	translation initia	1224	97.5	3.1	921	2	AE0332	conserved hypotet
1152	98.5	3.1	1764	2	B56101	collagen alpha 1(X	1225	97.5	3.1	929	2	T52517	hypothenical prote
1153	98.5	3.1	2180	2	T29764	hypothenical prote	1226	97.5	3.1	948	2	F87693	peptidase, M16 fam
1154	98.5	3.1	2339	2	A42566	omega-conotoxin-se	1227	97.5	3.1	1006	2	G86292	hypothenical prote
1155	98	3.1	182	2	T07641	PEARL1, 1 protein h	1228	97.5	3.1	1258	2	JC5765	inositol polyphosp
1156	98	3.1	291	2	AF0123	probable antigenic	1229	97.5	3.1	1392	2	T51947	probable transcrip
1157	98	3.1	296	2	A56943	sensory/motor neur	1230	97.5	3.1	1715	2	C40228	neurexin II-alpha
1158	98	3.1	303	2	S40973	hypothenical prote	1231	97.5	3.1	1748	1	JQ1555	genome polyprotein
1159	98	3.1	352	2	S09266	lg alpha chain C r	1232	97	3.1	191	2	F84522	probable proline-r
1160	98	3.1	416	1	A42879	advanced glycosyla	1233	97	3.1	238	2	T23867	hypothenical prote
1161	98	3.1	442	2	S50062	cell wall glycopro	1234	97	3.1	238	2	T26419	hypothenical prote
1162	98	3.1	499	2	A12449	hypothenical prote	1235	97	3.1	330	2	T05717	probable extensin
1163	98	3.1	514	2	A56201	transcription fact	1236	97	3.1	355	2	T26883	neural cell adhesi
1164	98	3.1	534	2	S21961	proline-rich prote	1237	97	3.1	357	2	A39364	GDF-1 embryonic gr
1165	98	3.1	535	2	S65762	chitinase (EC 3.2.	1238	97	3.1	379	2	AE3003	conserved hypotet
1166	98	3.1	538	2	I68092	PRR2 delta - human	1239	97	3.1	395	2	A86166	protein F21B7.6 [i
1167	98	3.1	538	2	A70836	hypothenical prote	1240	97	3.1	397	2	T00914	leucine-rich repea
1168	98	3.1	553	1	A42499	mullerian inhibiti	1241	97	3.1	400	1	A28172	spasmodysyn precu
1169	98	3.1	560	1	WFHUM	mullerian inhibiti	1242	97	3.1	421	1	S11674	acrosin (EC 3.4.21
1170	98	3.1	605	2	S48940	hypothenical prote	1243	97	3.1	428	1	TVHUEK	transforming prote
1171	98	3.1	614	2	S27962	modulator recognit	1244	97	3.1	452	2	D98280	hypothenical 28.0K
1172	98	3.1	631	2	C89243	protein F28C1.3 [i	1245	97	3.1	459	2	T35317	probable serine/th
1173	98	3.1	631	2	T21471	hypothenical prote	1246	97	3.1	483	2	T02226	NBS-LRR type resis
1174	98	3.1	715	2	S76492	lipoprotein nlpD -	1247	97	3.1	500	2	D97302	hypothenical prote
1175	98	3.1	728	2	H59435	phosphoinositide-3	1248	97	3.1	530	2	G70904	hypothenical prote
1176	98	3.1	750	2	T42614	probable envelope	1249	97	3.1	601	2	D89711	protein F40B10.4 [
1177	98	3.1	750	2	Q08583	HULFI protein - hu	1250	97	3.1	601	2	T22025	hypothenical prote
1178	98	3.1	856	2	T43631	serine/threonine k	1251	97	3.1	632	2	T02627	hypothenical prote
1179	98	3.1	889	2	C86257	resistance to pseu	1252	97	3.1	701	1	FOFV1R	gag polyprotein -
1180	98	3.1	896	2	S36326	clathrin assembly	1253	97	3.1	860	2	JC4566	chitinase (EC 3.2.
1181	98	3.1	1006	2	JC5526	kinase-defective E	1254	97	3.1	966	2	D96662	hypothenical prote
1182	98	3.1	1216	2	T34101	hypothenical prote	1255	97	3.1	967	2	G96637	kinase-related tra
1183	98	3.1	1372	2	T25933	hypothenical prote	1256	97	3.1	1123	2	A39962	disease resistance
1184	98	3.1	1522	2	H88380	protein T22F7.3 [i	1257	97	3.1	1214	2	T47438	neural cell adhesi
1185	98	3.1	1873	2	A55645	calcium channel, v	1258	97	3.1	1265	1	A37967	ATP dependent DNA
1186	98	3.1	2115	2	S38480	nonstructural prote	1259	97	3.1	1690	2	T35694	microtubule-associ
1187	98	3.1	3190	2	T13828	CREB-binding prote	1260	97	3.1	1734	2	A54602	hypothenical prote
1188	98	3.1	3623	2	T08618	intrinsic factor-B	1261	97	3.1	2055	2	T00093	genome polyprotein
1189	98	3.1	3635	2	T10053	laminin alpha 5 ch	1262	97	3.1	2205	1	GNVY2W	seven-pass transme
1190	98	3.1	3871	2	T22812	hypothenical prote	1263	97	3.1	3034	2	T14119	proline-rich prote
1191	98	3.1	5069	2	T17464	rifamycin polyketi	1264	96.5	3.1	346	2	S19129	peptidyl-prolyl ci
1192	97.5	3.1	215	2	S55925	probable arabinoga	1265	96.5	3.1	350	2	E75341	hypothenical prote
1193	97.5	3.1	266	1	A35037	insulin-like growt	1266	96.5	3.1	419	2	T40602	hypothetical prote
1194	97.5	3.1	268	2	S71830	transcription coac	1267	96.5	3.1	430	2	I48755	msAP1a - mouse
1195	97.5	3.1	277	2	A46241	interferon respons	1268	96.5	3.1	444	2	B36389	transcription fact
1196	97.5	3.1	306	2	T09067	extensin-like prote	1269	96.5	3.1	485	1	S22543	transcription fact
1197	97.5	3.1	338	1	TVMSFB	transforming prote	1270	96.5	3.1	487	2	F70765	hypothenical prote

1271	96.5	3.1	514	2	A31643	cell adhesion 80K	1344	95.5	3.0	1159	2	I38465	probable potassium
1272	96.5	3.1	528	2	B75310	conserved hypochet	1345	95.5	3.0	1255	2	T31065	diaphanous protein
1273	96.5	3.1	574	2	B35149	ipaH protein - Shi	1346	95.5	3.0	1356	2	T03096	CDO protein - rat
1274	96.5	3.1	598	2	T42070	protein serine/thr	1347	95.5	3.0	1331	2	T49813	related to gastric
1275	96.5	3.1	635	2	T70874	probable membrane	1348	95.5	3.0	1630	2	T00390	XIA0614 protein -
1276	96.5	3.1	637	2	A75342	hypothetical prote	1349	95.5	3.0	2761	2	T21064	hypothetical prote
1277	96.5	3.1	646	2	T34532	hypothetical prote	1350	95	3.0	175	2	I38408	neu differentiation
1278	96.5	3.1	654	2	T45017	chemotaxis histidi	1351	95	3.0	227	2	C29149	proline-rich prote
1279	96.5	3.1	669	2	T08827	hypothetical prote	1352	95	3.0	227	2	G70555	hypothetical prote
1280	96.5	3.1	796	2	E96654	hypothetical prote	1353	95	3.0	239	2	S25618	hypothetical prote
1281	96.5	3.1	825	1	EDBEXD	immediate-early pr	1354	95	3.0	241	2	D43273	heretulin precursor
1282	96.5	3.1	1021	2	A86421	Receptor-like seri	1355	95	3.0	273	2	C70551	hypothetical prote
1283	96.5	3.1	1209	2	T00373	hypothetical prote	1356	95	3.0	326	2	A59232	ABA-responsive pro
1284	96.5	3.1	1241	2	T18311	hypothetical prote	1357	95	3.0	338	2	T06336	proline-rich prote
1285	96.5	3.1	1557	2	T02859	probable serine/th	1358	95	3.0	385	1	I39498	GTP cyclohydrolase
1286	96.5	3.1	2282	2	T42717	DNA-binding protei	1359	95	3.0	413	2	T52617	hypothetical prote
1287	96.5	3.1	2352	2	T30201	Notch homolog prot	1360	95	3.0	477	2	S53362	mucin 5AC (clone J
1288	96.5	3.1	26926	1	I38344	titin, cardiac mus	1361	95	3.0	494	1	A29079	lymphocyte surface
1289	96	3.1	214	2	T10737	extensin-like cell	1362	95	3.0	502	2	A55197	Wiskott-Aldrich sy
1290	96	3.1	240	2	A24264	proline-rich prote	1363	95	3.0	636	2	I61718	neu differentiation
1291	96	3.1	287	2	C75494	cell division prot	1364	95	3.0	653	2	E84682	hypothetical prote
1292	96	3.1	346	2	TJ0159	cysteine proteinas	1365	95	3.0	662	2	I61722	neu differentiation
1293	96	3.1	445	2	T05887	hypothetical prote	1366	95	3.0	667	2	T17221	hypothetical prote
1294	96	3.1	451	2	D88395	protein F53A3.6 [1	1367	95	3.0	673	2	T48012	hypothetical prote
1295	96	3.1	483	2	S12741	transcription fact	1368	95	3.0	705	2	A35621	spore germination
1296	96	3.1	537	1	FMVGV	gag polyprotein -	1369	95	3.0	712	2	G02512	interleukin-1 rece
1297	96	3.1	580	2	T43481	probable mucin DKP	1370	95	3.0	760	2	T16726	hypothetical prote
1298	96	3.1	594	2	S33561	ref(2)P protein -	1371	95	3.0	776	2	C96554	unknown protein [i
1299	96	3.1	598	2	T48822	hypothetical prote	1372	95	3.0	799	2	T48889	serine/threonine p
1300	96	3.1	635	1	WMBE66	capsid protein - h	1373	95	3.0	846	2	S52418	GTP-binding regula
1301	96	3.1	858	1	IJRTNC	neural cell adhesi	1374	95	3.0	891	2	G84693	probable proline-r
1302	96	3.1	883	2	A96662	hypothetical prote	1375	95	3.0	901	2	A44825	phosphoprotein, sy
1303	96	3.1	907	2	AD2951	cell division prot	1376	95	3.0	903	2	S60257	meltrin alpha - mo
1304	96	3.1	910	2	H98331	cell division prot	1377	95	3.0	943	2	T34847	probable transcrip
1305	96	3.1	969	2	A75634	McR8-related prote	1378	95	3.0	1024	2	S18251	collagen alpha 1(X
1306	96	3.1	1216	2	T26104	hypothetical prote	1379	95	3.0	1209	2	T13153	brahma associated
1307	96	3.1	1231	2	S30185	insulin receptor s	1380	95	3.0	1324	2	T14070	peptide synthetase
1308	96	3.1	1544	2	E59431	phosphoinositide-b	1381	95	3.0	1474	2	B85188	retrotransposon li
1309	96	3.1	1615	2	B49502	protein-tyrosine-p	1382	95	3.0	1616	2	G70668	polyketide synthas
1310	96	3.1	1737	2	T00209	MGF8 protein - hu	1383	95	3.0	1731	2	AB3045	ice nucleation pro
1311	96	3.1	1767	2	A49502	protein-tyrosine-p	1384	95	3.0	1731	2	B98241	hypothetical prote
1312	96	3.1	1844	1	RRWPTM	genome polyprotein	1385	95	3.0	1770	2	T18551	saframycin Mxi syn
1313	96	3.1	2529	2	A56923	transcription fact	1386	95	3.0	1806	1	CGHUIE	collagen alpha 1(X
1314	96	3.1	5376	2	T42215	zonadhesin - mouse	1387	95	3.0	2090	2	T30075	hypothetical prote
1315	95.5	3.0	188	2	D29149	proline-rich prote	1388	95	3.0	2148	2	A56011	transcription fact
1316	95.5	3.0	284	2	F95520	conserved hypochet	1389	95	3.0	2274	2	T30258	adenomatous polyo
1317	95.5	3.0	366	1	TDMSN4	monocyte surface g	1390	95	3.0	3084	1	MMMSA	laminin alpha-1 ch
1318	95.5	3.0	382	2	S75823	threonine synthase	1391	94.5	3.0	211	2	T03381	high sulfur zein p
1319	95.5	3.0	384	2	S51796	vasodilator-stimul	1392	94.5	3.0	255	2	B75309	hypothetical prote
1320	95.5	3.0	435	2	T46443	hypothetical prote	1393	94.5	3.0	255	2	S31096	proline-rich prote
1321	95.5	3.0	451	2	S71754	cellular hepatitis	1394	94.5	3.0	270	2	E87649	hypothetical prote
1322	95.5	3.0	479	2	D70676	probable PE protei	1395	94.5	3.0	277	2	I38857	microtubule-associ
1323	95.5	3.0	486	2	AB2975	succinate semialde	1396	94.5	3.0	298	2	H87533	peptidase, M23/M37
1324	95.5	3.0	486	2	A98308	atrk protein (U594	1397	94.5	3.0	301	2	D87684	transcription regu
1325	95.5	3.0	501	2	S76563	hypothetical prote	1398	94.5	3.0	358	2	A61188	probable transcrip
1326	95.5	3.0	507	1	A46711	erythropoietin rec	1399	94.5	3.0	376	2	H82988	hypothetical prote
1327	95.5	3.0	553	2	C75318	hypothetical prote	1400	94.5	3.0	393	2	E82283	conserved hypochet
1328	95.5	3.0	570	2	A48836	fibropellin C prec	1401	94.5	3.0	464	2	A83557	probable amidease p
1329	95.5	3.0	571	2	T43356	hypothetical prote	1402	94.5	3.0	569	2	T19128	hypothetical prote
1330	95.5	3.0	573	2	B70726	probable secD - My	1403	94.5	3.0	630	2	A39344	tumor-associated m
1331	95.5	3.0	624	2	T49366	myocyte-specific e	1404	94.5	3.0	665	2	E75461	probable cell wall
1332	95.5	3.0	630	2	T31798	hypothetical prote	1405	94.5	3.0	708	2	JC4364	gelatinase B (EC 3
1333	95.5	3.0	650	2	S44806	FlO89.6 protein -	1406	94.5	3.0	719	2	T33170	hypothetical prote
1334	95.5	3.0	685	2	C56591	E75 B steroid rece	1407	94.5	3.0	860	2	I48839	tanascin-X - mouse
1335	95.5	3.0	710	1	S70965	serine/threonine-s	1408	94.5	3.0	921	2	S42617	collagen alpha 1(I
1336	95.5	3.0	722	2	T22359	hypothetical prote	1409	94.5	3.0	985	2	T06049	hypothetical prote
1337	95.5	3.0	749	2	E87599	hypothetical prote	1410	94.5	3.0	1006	2	TJ0050	hypothetical prote
1338	95.5	3.0	790	1	TVHUTT	narve growth facto	1411	94.5	3.0	1092	1	JN0635	neural cell adhesi
1339	95.5	3.0	880	2	D89756	protein T2387.2b l	1412	94.5	3.0	1191	2	T13850	gene u-shaped prot
1340	95.5	3.0	943	2	E84429	probable receptor-	1413	94.5	3.0	1487	1	EDBEE1	immediate-early pr
1341	95.5	3.0	943	2	A54092	protein-tyrosine k	1414	94.5	3.0	1690	1	CGHUIB	collagen alpha 4(I
1342	95.5	3.0	1027	2	I38759	zinc finger/leucin	1415	94.5	3.0	2062	2	G96602	probable receptor
1343	95.5	3.0	1054	2	A30239	hydroxymethylgluta	1416	94.5	3.0	2302	2	T14328	protein-tyrosine-p

1417 94.5 3.0 2386 1 FNHU 1 fibronectin precu
1418 94.5 3.0 2484 2 T26216 2 hypothetical prote
1419 94.5 3.0 2607 2 T26215 2 hypothetical prote
1420 94 3.0 157 2 T2034 2 early light-induce
1421 94 3.0 263 2 S57346 2 interleukin 15 rec
1422 94 3.0 277 2 T22564 2 hypothetical prote
1423 94 3.0 293 2 T22919 2 hypothetical prote
1424 94 3.0 329 2 T10064 2 cytokinin-induced
1425 94 3.0 338 2 S28004 2 probable cell surf
1426 94 3.0 346 2 T69233 2 hypothetical prote
1427 94 3.0 356 2 A96826 2 T8K14.10 importe
1428 94 3.0 421 2 T38309 2 probable cell wall
1429 94 3.0 456 2 A40492 2 early growth respo
1430 94 3.0 466 2 A36389 2 transcription fact
1431 94 3.0 476 2 B44997 2 merozoite surface
1432 94 3.0 522 2 S41819 2 nucleoporin p62 -
1433 94 3.0 559 2 C75286 2 hypothetical prote
1434 94 3.0 590 2 B36789 2 hypothetical prote
1435 94 3.0 639 2 I61719 2 neu differentiatio
1436 94 3.0 648 2 S50856 2 wnn protein - rat
1437 94 3.0 677 2 JC7303 2 pectate lyase (EC
1438 94 3.0 693 1 A41090 2 serine/threonine-s
1439 94 3.0 791 2 S67265 2 hypothetical prote
1440 94 3.0 811 2 T36581 2 probable transmem
1441 94 3.0 862 2 S51493 2 major nitrogen reg
1442 94 3.0 865 1 D70986 2 probable ABC trans
1443 94 3.0 898 2 A40114 2 interleukin-3 rece
1444 94 3.0 918 2 JC4361 2 scavenger receptor
1445 94 3.0 927 2 A48085 2 transcription fact
1446 94 3.0 939 2 C70876 2 hypothetical prote
1447 94 3.0 979 2 A70848 2 probable membrane
1448 94 3.0 1007 2 G96606 2 disease resistance
1449 94 3.0 1137 2 G70868 2 probable regulator
1450 94 3.0 1236 2 E70977 2 hypothetical prote
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1452 94 3.0 1331 2 A48954 2 mannan endo-1,4-be
1453 94 3.0 1335 2 T18289 2 racGAP protein - s
1454 94 3.0 1429 2 T13720 2 gene expanded prot
1455 94 3.0 1549 2 T11974 2 glutamate synthase
1456 94 3.0 1560 2 T00080 2 hypothetical prote
1457 94 3.0 2153 2 T30074 2 hypothetical prote
1458 94 3.0 172 2 D41132 2 collagen-related p
1459 93.5 3.0 278 2 T27610 2 hypothetical prote
1460 94 3.0 299 2 G70784 2 probable mmp3 pro
1461 94 3.0 305 2 T46721 2 hypothetical prote
1462 94 3.0 352 2 T06482 2 probable cell wall
1463 94 3.0 362 2 S61824 2 cyst wall protein
1464 93.5 3.0 391 2 I50702 2 transcription fact
1465 93.5 3.0 458 2 B87335 2 hypothetical prote
1466 93.5 3.0 461 1 A35356 2 tumor necrosis fac
1467 93.5 3.0 480 2 AG1107 2 internalin G limpo
1468 93.5 3.0 522 2 T36501 2 probable serine/th
1469 93.5 3.0 530 2 A53437 2 poliovirus recepto
1470 93.5 3.0 556 2 T42100 2 serine/threonine p
1471 93.5 3.0 577 2 T18116 2 hypothetical prote
1472 93.5 3.0 662 2 T46005 2 receptor-like prot
1473 93.5 3.0 691 2 B75622 2 hypothetical prote
1474 93.5 3.0 718 2 T05840 2 subtilisin-like pr
1475 93.5 3.0 719 2 F96577 2 hypothetical prote
1476 93.5 3.0 854 2 A66574 2 protein F12M16.30
1477 93.5 3.0 909 1 QRXLL2 2 LDL receptor 2 pre
1478 93.5 3.0 919 2 F83257 2 hypothetical prote
1479 93.5 3.0 998 2 T3745 2 probable ATP-bind
1480 93.5 3.0 1121 2 JC7329 2 WD-repeat protein
1481 93.5 3.0 1209 2 B89066 2 protein H05009.1
1482 93.5 3.0 2109 2 T33247 2 hypothetical prote
1483 93.5 3.0 2150 2 T32497 2 hypothetical prote
1484 93.5 3.0 2295 2 C88369 2 protein unc-52 lim
1485 93.5 3.0 3375 2 T19821 2 hypothetical prote
1486 93.5 3.0 209 2 T02262 2 high-methionine d-
1487 93 3.0 221 2 T07079 2 leucine-rich repea
1488 93 3.0 235 2 PC2022 2 mucin like protein

1490 93 3.0 328 2 S01359 2 salivary glue prot
1491 93 3.0 338 2 S38030 2 suppressor protein
1492 93 3.0 384 2 H70580 2 hypothetical prote
1493 93 3.0 413 2 AH2743 2 conserved hypotet
1494 93 3.0 416 2 G97524 2 hypothetical prote
1495 93 3.0 438 2 G87675 2 arylesterase-relat
1496 93 3.0 453 2 B42093 2 serum response fac
1497 93 3.0 465 2 B82515 2 alpha-L-fucosidase
1498 93 3.0 558 2 T50742 2 protoporphyrin IX
1499 93 3.0 560 1 JC4795 2 plasma hyaluronan-
1500 93 3.0 586 2 H86914 2 conserved hypotet

RESULT 1
JC5239
insulin-like growth factor acid-labile chain - baboon
C;Species: Papio sp. (baboon)
C;Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
C;Accession: JC5239
R;Delhanty, P.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 227, 897-902, 1996
A;Title: The cloning and expression of the baboon acid-labile subunit of the insulin-like
A;Reference number: JC5239; MUID:97040714; PMID:8886027
A;Contents: liver
A;Accession: JC5239
A;Molecule type: mRNA
A;Residues: 1-605
A;Cross-references: UNIPARC:UPI000000D50E
C;Comment: This factor is structurally related to proinsulin and have insuline-like metal

Query Match 10.3%; Score 322; DB 2; Length 605;
Best Local Similarity 36.2%; Pred. No. 2e-11;
Matches 100; Conservative 39; Mismatches 97; Indels 40; Gaps 11;
QY 7 LLLPLLLL--LAIG-----PGVOG-----CPGCGCQSQPQ-----TVFTARQGIT 45
DB 8 LALALLLSWALGPRSLGAEFGTPEGAEPACATCACSYDDEVNELSVFCSSRLNR 67
QY 46 VPRDVPDVTGLVVFENGITMLDASSFAGLPGIQLLDLSQNOIASLRLLPRLLL----- 98
DB 68 LPDIPGGTQALWLDNSNLSIPPAAFRNLSSLAFLNQQGQGSLE-POALLGLENLCH 126
QY 99 LQLSHNSLLALPGILDITANVEALRLAGLG---LQQLDEGLFSRLRLHDLVDSDNQLER 155
DB 127 LHLERNQLSLAVGTF--AYTPALALLGLSNNRLSRLEDGLFGLGNLWDLNGLNSLAV 184
QY 156 VP-PVIRGLRGLTRLRAGNTRIAQLRPBDELGLAALQELDVNSLSLOALPGDLSGLFPR 214
DB 185 LPDAFRGLGGLRELVLGN-RLAYLQPALFSGLAELRELDLSRNALRAIKANVFAQLPR 243
QY 215 LRLAARNPFCVCPLSWFG----PWVRESHVTLA 246
DB 244 LQKLYLDRNLIAAVAFGLGLKALRWLDLSHNRVA 279

RESULT 2
A41915
insulin-like growth factor-binding complex acid-labile chain precursor - human
N;Alternate names: Acid-Labile Subunit (ALS)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A41915
R;Leong, S.R.; Baxter, R.C.; Camerato, T.; Dai, J.; Wood, W.I.
Mol. Endocrinol. 6, 870-876, 1992
A;Title: Structure and functional expression of the acid-labile subunit of the insulin-l
A;Reference number: A41915; MUID:92357025; PMID:1379671
A;Accession: A41915
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-605 <LEO>

A;Cross-references: UNIPROT:P35858; UNIPARC:UPI000000088A; GB:M86826; NID:g184807; PIDN:
A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIP:110171)
F;75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
F;315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
F;339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
F;363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
F;387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
F;411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
F;435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
F;459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR17>
F;483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR18>
F;507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR19>

Query Match 9.6%; Score 302; DB 2; Length 605;
Best Local Similarity 35.5%; Pred. No. 2.9e-10;
Matches 98; Conservative 40; Mismatches 98; Indels 40; Gaps 11;

Qy 7 LLLPLLLL--LALG-----PQVQ-----CPSGCQCSQ-----TVFCTARQGT 45
Db 8 LALLLLSVALGPRLEGADPTGEARGPACVCSYDDADELSVFCSSNLR 67

Qy 46 VPRDVPDTVGLYFENGITMLDASSPAGLPGLQLDLDSQNASLRPLRL-- 98
Db 68 LPDGVPGTQALMDGNLSSVPPAFQNLSSGLFLNLQGGQLGSL-PPALLGLENLCH 126

Qy 99 LLSHNSLLALEPGILDANVEALRLAGL---LQDDEGLFSRLRLNHLVDSDNQLER 155
Db 127 LHLERNQLSLALGTF--AHTPALASLGSNNRSLRLEDGLFEGSLGSLWDLNLGWSLAV 184

Qy 156 VP-VPTVRLGLFRLRAGNTRTAQLRPEDLAGLAQLQELDVNSLQALPGDLSGLFPR 214
Db 185 LPDAAFRGLSGLRELVLVAGN-RLAYLQFALFSGLAELRLDLSRNALRAIKANVFQVLR 243

Qy 215 LRLLAARNPFCVPLSWFG-----PMVRESHVTLA 246
Db 244 LQKLYLDRLNLAIVAPGAFGLKALRLDLDSHNRVA 279

RESULT 3
NBHUIA
platelet glycoprotein Ib alpha chain precursor - human
N;Alternate names: membrane glycoprotein Ib alpha chain
N;Contains: glycosialin
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence, revision 28-Dec-1987 #text change 09-Jul-2004
C;Accession: A94174; S16945; A94173; S16945; I55355; A27075; A27102
R;Lopez, J.A.; Chung, D.W.; Fujikawa, K.; Hagen, F.S.; Papayannopoulou, T.; Roth, G.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 5615-5619, 1987
A;Title: Cloning of the alpha-chain of human platelet glycoprotein Ib: a transmembrane p
A;Reference number: A94174; MUID:87289654; PMID:3303030
A;Accession: A94174
A;Molecule type: mRNA
A;Residues: 1-626 <LQ>
A;Cross-references: UNIPROT:P07359; UNIPARC:UPI0000128962; GB:J02940; NID:g183499; PIDN:
R;Wickl, A.N.; Walz, A.; Gerber-Huber, S.N.; Wenger, R.H.; Vornhagen, R.; Clemetson, K.J.
Thromb. Haemost. 61, 448-453, 1989
A;Title: Isolation and characterization of human blood platelet mRNA and construction of
d cloning of a GPIb coding cDNA insert.
A;Reference number: A60435; MUID:90020160; PMID:2799758
A;Accession: A60435
A;Molecule type: mRNA
A;Residues: 207-467 <WIC>
A;Cross-references: UNIPARC:UPI0000174311

R;Titani, K.; Takio, K.; Handa, M.; Ruggeri, Z.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 5610-5614, 1987
A;Title: Amino acid sequence of the von Willebrand factor-binding domain of platelet mem
A;Reference number: A94173; MUID:87289654; PMID:3497398
A;Accession: A94173
A;Molecule type: protein
A;Residues: 17-315 <TIT>
A;Cross-references: UNIPARC:UPI0000174312
R;Hess, D.; Schaller, J.; Rickli, E.E.; Clemetson, K.J.
Eur. J. Biochem. 199, 389-393, 1991
A;Title: Identification of the disulphide bonds in human platelet glycosialin.
A;Reference number: S16945; MUID:91301149; PMID:2070794
A;Accession: S16945
A;Status: preliminary
A;Molecule type: protein
A;Residues: 224-227/262-270/277-282 <HES>
A;Cross-references: UNIPARC:UPI0000174313; UNIPARC:UPI0000174314; UNIPARC:UPI0000174315
R;Lopez, J.A.; Ludwig, E.H.; McCarthy, B.J.
J. Biol. Chem. 267, 10055-10061, 1992
A;Title: Polymorphism of human glycoprotein Ib alpha results from a variable number of t
atons.
A;Reference number: I55355; MUID:92250564; PMID:1577776
A;Accession: I55355
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 412-427 <RES>
A;Cross-references: UNIPARC:UPI000073621; GB:S34436; NID:g249176; PIDN:AAB22152.1; PID:
A;Note: variant D
C;Comment: Glycoprotein Ib (GPIb), a surface membrane protein of platelets, participates
C;Comment: Platelet activation apparently involves disruption of the macromolecular comp
C;Comment: Binding sites for von Willebrand factor and thrombin (the latter site with un
C;Comment: Glycosialin, which is approximately coextensive with the extracellular part
C;Genetics:
A;Gene: GDB:GP1BA; GP1B
A;Cross-references: GDB:118806; OMIM:231200
A;Map position: 17pter-17p12
C;Complex: heterodimer with platelet glycoprotein Ib beta chain (NBHUIB)
C;Superfamily: platelet glycoprotein Ib alpha chain; leucine-rich alpha-2-glycoprotein re
C;Keywords: blood coagulation; duplication; glycoprotein; platelet membrane; tandem repe
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-626/Product: platelet glycoprotein Ib alpha chain #status predicted <MPT>
F;48-71/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;72-93/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;94-116/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;117-140/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;141-164/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;165-188/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;189-212/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;379-430/Region: proline/threonine-rich 9-residue repeats
F;502-540/Domain: transmembrane #status predicted <TRM>
F;541-626/Domain: intracellular #status predicted <INT>
F;37,175/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;308/Binding site: carbohydrate (Thr) (covalent) #status experimental

Query Match 9.0%; Score 282; DB 1; Length 626;
Best Local Similarity 24.0%; Pred. No. 4.4e-09;
Matches 160; Conservative 72; Mismatches 244; Indels 190; Gaps 26;

Qy 9 LPLLLLLGPVGQCGSCQCSQPT---VFCTARQGTTPRDVPPDTVGLYFVN--- 62
Db 1 MPLLLLLLLLPSPLPHPICEVSKVASHLEVNCDEKNTALPPDLPKDTTILHLENLLY 60

Qy 63 -----GTMLDASSF-----AGLPGLQLDLDSNQIASL-----RLPRLLL 98
Db 61 TFSLATLMPYTRUTQUNLDRCELTUKVDGTLFVLGTLDSHNQLSPLLGQTLPALTV 120

Qy 99 LLSHNSLLALEPGIL-DTANVEALRLAGLQDLDEGLFSRLRLNHLVDSDNQLERVP 157
Db 121 LDVSNRLTSLPLGALRGLGELQELYLKGNELKTLPPGLLTPTPKLEKLSLANNLTLP 180

Qy 158 P-VIRGLGLTRLRAGNTRIAQLRPEDLAGLAQLQELDVNSLQALPGDLSG--LFP 214
Db 181 AGLINGLENLDTLLQEN-----SLYTIKPFPGSHLLPF 215

Qy	215	LRLAAARNPNCVCLPSWFGPWRES-----HVTLASPEETRC-----	253
		:: :: :: :::::	:
Db	216	AFLHG---NPWLNCNCEILYFRRWLQDCAENVVVKQGVDKAMTNNVASVOCDNSDKFPV	272
Qy	254	-HFPPKNAGRILLE--LDYADFGCPATTTATVPTRPVVRP-----TA	295
Db	273	YKYFGKGCPTLGDEGDTLDYYIPEEDTEGDVKVRATRIVVKFPTKAHTTPWGLFYSWSTA	332
Qy	296	LSSSLAPFWLSPTAPATE-----ABSPSTAPPTVGVP---PQ	330
Db	333	SLDSQMPSLSHPTOBSTKEQTTFPPRPWPNFNLHMESITFSXPKSTTEPTSPSTSEPV	392
Qy	331	PQDCPPSPCLANGGTCHLGRHHIACLCPGFGLCYCSQMGGOTRPSPTVPTRPPRSUT	390
Db	393	PEPAPNMTTLEPTP-----STTPE-----PTSEPASPPTTPEPTPIPT	431
Qy	391	LGIBP---VSPTSURVLQRYLOQSS--VOLRSRLTYRNLSGDPDKRLVTLR--LPASIA	443
Db	432	IATSFTILVSATSLITPKSTFLTTPKVPSLLESTKKTIPELLQPCKPLRGVLQCHLESSRN	491
Qy	444	EYTVQLBPNTATYSVCVMPLG-----PGEV-PEGEEACGEAHT	480
Db	492	D---PFLHPD---FCCLPLPLGYLVGLFWLLPASVVLILLJLSWGWHVKPQALDSOGGAAL	545
Qy	481	PPAVHSNHAPVTQAREGNLP---LLI----APALAAVLLAALAAVGAAYCVRRGRAMAAA	533
Db	546	TTAQTQTHLELQRGOVTPRAWLLFLRGSLPTFRSSLFWTRPNRNGRVCPVAGRRPSAL	605
Qy	534	AQDKGO	539
Db	606	SQGRGO	611

RESULT 4

insulin-like growth factor-binding protein acid labile chain precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: JCI1282
R/Dai, J.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 188, 304-309, 1992
A/Rittle: Molecular cloning of the acid-labile subunit of the rat insulin-like growth fac
A/Reference number: JCI1282; MUID:93038676; PMID:11384485
A/Accession: JCI1282
A/Molecule type: mRNA
A/Residues: 1-603 <DAI>
A/Cross-references: UNIPROT:P35859; UNIPARC:UPI0000125918; GB:S46785; NID:g258002; PIDN:
A/Experimental source: liver
A/Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205
F/1-27/Domain: signal sequence #status predicted <SIG>
F/28-603/Product: insulin-like factor binding protein, acid labile chain #status
F/267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 9.0%; Score 281.5; DB 2; Length 603;
Best Local Similarity 32.4%; Pred. No. 4.5e-09;
Matches 92; Conservative 49; Mismatches 106; Indels 37; Gaps 11;

Qy 6 PLLPLLLL-LALGP-QVGQ-----CPSCQCQSQPQ-----TVFCTARQGT 45
Db 8 PALVVLLAFWALGPCHLQGTDFGASADAEGPQCPVACTCHDDYTDLSVFCSSKNLTH 67
Qy 46 VPRDVPDPTGVLVYFENGITWLDASSFAGLPGIQLDLSONQIASLR-----LPRLLLL 99
Db 68 LPDDIPVSTRALWIDGNLSSIPSAFQNLSSLDFLNLQGSWLRSLPEQALLGLQNLYYL 127
Qy 100 DLSHNSLLALEPGTL-DTANVEALRLAGLGLQQLDEGLFSRLRLNLHDLVDSDNQLERVP- 157
Db 128 HLENRRLNLAUGLFTTTPSLASLSLSNLLGRLEGLFGCLSHLWDLNLGNWSLVLPD 187
Qy 158 PVIRGLGLTRLRIAGNTRIAQLRPEDLAGLAALQELDVSNLSIQALPGDLGLFPRLRL 217
Db 188 TVFGIQLNHLVLVAGN-KLTYLOPALFCGLGELRELDLSRNALRSVKANVFVHLPRLOK 246

RESULT. T 6

Accession: T42218
 Description: slit-1 protein homolog - rat
 N:Alternate names: MEGF4 protein
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T42218
 E:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O. Genomics 51, 27-34, 1998
 A:Title: Identification of high-molecular-weight proteins with multiple EGF A:Reference number: Z14126, MUID:98360089; PMID:9693030
 A:Accession: T42218
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1531 <NAK>
 A:Cross-references: UNIPROT:O88279; UNIPARC:UPI000004F20B; EMBL:AB011530; N A:Experimental source: strain Sprague-Dawley; brain
 C:Genetics:
 A:Gene: MEGF4
 C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-g
 Query Match 8.9%; Score 278; DB 2; Length 1531;
 Best Local Similarity 25.8%; Pred. No. 2.1e-08;

Matches 127; Conservative 56; Mismatches 207; Indels 102; Gaps 16;

QY 6 PLLPLLLALLGAGVQGCSCGCSQPTVCTARQTTVPDRVDPDTVGLVVFENGIT 65
DB 16 PELWLLAAARLIGATACALCTCT-GTTVDCHGTGLQAIPIKNIPTNTERLENGNIIT 74
QY 66 MLDASSFAGLPGIQLLDLSQNIASLRLLLDLSHNSLLALEPGIL-DTANVEALRL 124
DB 75 RIHKNDPAGLKQLRVLQLMENQIG-----AVERGAPDDMKELERLRL 116
QY 125 AGIQLQOLDGLSRSLRNLHDLVDSDNQLERVP-PVIRGLRGLTRLRLAGNTRIAQLRPE 183
DB 117 NRNLQQLVPELLFQNNQALSRLLDLSNSLQAVPRKAFRGATDLKQLQLDKN-QISCTIEG 175
QY 184 DLAGLAALQELVDNSLSQALPGDLSGLFPRRLILAAARNPFCVPLSWFGFWVRESHV 243
DB 176 AFRLALRGLEVLTNNNNITIPVSSFNHMPKLRTRFLHSNHLFCDCHLAWLSQWLQ-RP 234
QY 244 TLASPEETRCHFPKPNAGRLLELDYADFQCPATTTTATVPTTRPVVREPTALSSSLAPT 303
DB 235 TIGL--FTQCSGPASLRGLNVAEVQKSEFSCSGGEEAQPVA-----CTLSSGSCPA 284
QY 304 WLSFTAPATAPSPPTAPTPVGPVPOQ-----DCPSTCLNGTCHLG----- 348
DB 285 MCSCSNGIVDCRGKGLTAIPANLPETMTTEIRLELNGIKSIPP-----GAFSPYR 333
QY 349 -----TRHHLACLCEGFTGLYCSESQMGTRPSTVTPRPRSLTLGIBPVS--PT 399
DB 334 KLRRIDLSNNQIAEIPADFQGL-----RSLNSLVLYGNKTIIDLPR 374
QY 400 SLRVLGQRYLQGGSSVQLSRRLTRNLSGPD--KRLVTLRLPA-----SLAEYTVTQL 450
DB 375 GVFGGLY-----TLQLLLLNANKINCIRPDQDLQNLSSLYNDNKIQSLAKGFTSL 428
QY 451 RPNATYSVCVMP 462
DB 429 RAIQTLLHAQNP 440

RESULT 7
A53531
oncofetal trophoblast glycoprotein 574 precursor - human
N;Alternate names: oncofetal antigen 574
C;Species: Homo sapiens (man)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: A53531.48087
R;Myers, K.A.; Rahi-Saund, V.; Davison, M.D.; Young, J.A.; Cheater, A.J.; Stern, P.L.
J. Biol. Chem. 269, 9319-9324, 1994
A;Title: Isolation of a cDNA encoding 574 oncofetal trophoblast glycoprotein. An antigen
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-420/Product: oncofetal trophoblast glycoprotein 574 #status predicted <MAT>

Query Match 8.4%; Score 264.5; DB 2; Length 420;
Best Local Similarity 28.1%; Pred. No. 2.9e-08;
Matches 103; Conservative 44; Mismatches 121; Indels 99; Gaps 15;

QY 2 CSRV-----LLPLLLLLALG-----PQVQCPS 26
DB 5 CSRGAAGDGLRLRLALVLLGVSSSSPTSSASSFSAPFLASAVSQPLPDQCPA 64
QY 27 GCOCSSQ--PQTVCTARQTTVPDRVDPDTVGLVVFENGITMLDASSFAGLP---GLQLLD 82
DB 65 LCFCSEAAATVCKVNRNLTEVPTDLPAYVNRNLFTGNQLAVLPAGAFARRPPPLAEALN 124
QY 83 LSONQTASLR-----LPRLLLDLSHNSLLALEPGILDPTANVEALRLAGLQQLDEGL 136

DB 125 LSGSRLEVRAGAFEHLPSLRQLDLSHNLADLSPFAFGSNASV-----SAPSP 175
QY 137 FFSRLRLHDLVDSDNQLER-----VPPVI--RGLRGLTRLRLAGNTRIAQLRPEDLAGL 188
DB 176 VELILN-HIVPPEDEQRNSFEGVVAALLAGRALQGLRLELASN-HFLYLPDRDVLQAL 233
QY 189 AALQELVDNSLSQALP-----GDLGLFPRRLRLAA 220
DB 234 PSURHLDSNLSVSLTVYVFRNLTHLESJLHLEDNALKVLHNGTLAELOGL-PHIRVF-L 291
QY 221 ARNPFNCVCLPSWFGFWVRESHVTLASPEETRCHFPKPNAGRLLELDYADFQ-----PA 276
DB 292 DNNPVCDDCHMADMTWLKETEV-VQGRKRLTCAYPEKMRNRVLELNSADLDCDPLPP 350
QY 277 TTTTATV 283
DB 351 SLOTSV 357

RESULT 8
T13953
MEGF5 protein - rat
N;Alternate names: slit protein homolog
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13953
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A;Reference number: Z14126; MUID:98360089; PMID:9693030
A;Accession: T13953
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1523 <NA>
A;Cross-references: UNIPROT:O88280; UNIPARC:UPI0000085F7A; EMBL:AB011531; NID:93449291; I
C;Gene: MEGF5
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r

Query Match 8.3%; Score 261; DB 2; Length 1523;
Best Local Similarity 26.3%; Pred. No. 2e-07;
Matches 93; Conservative 41; Mismatches 126; Indels 94; Gaps 14;

QY 24 CPSCGCSQPTVCTARQTTVPDRVDPDTVGLVVFENGITMLDASSFAGLPGLQLLDL 83
DB 725 CPQCCTCV--TVVRCNSRGLHTLPKMPKDVTELYLEGNHLTAV----- 767
QY 84 SQNQIASLRRLRLDLLDLSHNSLLALEPGILDPTANVEALRLAGLQQLDEGLFSRLNL 143
DB 768 -PKELSTFR--QLTLIDLSSN-----ISMLTNHTFSSNMSHL 801
QY 144 HDLDVSDNQLERVP-PVIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELVDNSLSLQ 202
DB 802 STLILSYNRLRCLPIVHAFNGLRSRLVTLHGN-----DISSVPEGSFNDLTSLS-- 850
QY 203 ALPGDLSGLFPRRLILAAARNPNCVPLSWFGFWVRESHVTLASPEETRCHFPKPNAGR 262
DB 851 -----HLALGINPLHCDCLSEWSEWIKAGY---KEFGIARCSSPESNADR 893
QY 263 LLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWSLPTAPATEAPSPSTAP 322
DB 894 LLLTTPTRFOCKG-----PVDINIVAKCNACLSS--PCKNGTCSQDPVEQYRCTCP 944
QY 323 PTVGVPVQDQC--PPSTCL-----NGGTCHLGRHH--LACLCPGEGFTGLYCE 367
DB 945 YSY-----KGKDOCTVPINTCVQNPQGGTCHLSHSDRGFSCPLGFEGQRC 994

RESULT 9
B36665
slit protein 2 precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002

C;Accession: B36665
R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A;Title: slit: an extracellular protein necessary for development of midline glia and cell
A;Reference number: A36665; MUID:91099665; PMID:2176636
A;Accession: B36665
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1469 <ROT>
A;Cross-references: UNIPARC:UPI0000177454; GB:X53959
C;Genetics:
A;Gene: FlyBase:sl
A;Cross-references: FlyBase:FBgn0003425
C;Superfamily: proteoglycan amino-terminal homology <PAH1>
F;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>
F;288-313/Domain: proteoglycan amino-terminal homology <PAH2>
F;323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
F;450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>
F;512-537/Domain: proteoglycan amino-terminal homology <PAH3>
F;547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
F;572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
F;596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
F;620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
F;651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>
F;708-733/Domain: proteoglycan amino-terminal homology <PAH4>
F;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
F;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
F;846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
F;1028-1061/Domain: EGF homology <EGF>
F;1068-1099/Domain: EGF homology <EGF2>
F;1115-1148/Domain: EGF homology <EGF1>
Query Match 8.1%; Score 255.5; DB 2; Length 1469;
Best Local Similarity 21.4%; Pred. No. 3.9e-07;
Matches 105; Conservative 52; Mismatches 168; Indels 165; Gaps 14;
QY 24 CPSCGCSQPTVFCTARQCTTPRDPV-----PDTVGLY 58
DB 519 CPANCHC-EGTVDCGRRRLKEIPDILPHLTTELLNDNDELGRISDGLFGRPLHLVKLE 577
QY 59 VFENGITMLDASSFAGLPGQLLDLSONQIAS-----LRLPRLLDLSDHNSLLALEPG 112
DB 578 LKENQLTGTPNAFEGASHIQELQGENKIKEISNMFLGLHQLKTLNLYDNQISCVMPG 637
QY 113 ILDTAN-----VEALRLAGLGLQQLDGLFSRLNHLHDV--- 148
DB 638 SFPHLSLTLNLASPNFNCNCHLAWFAECVRKSLNGGAARCAPSKVRDVQIKDLPHS 697
QY 149 -----SDNQLERVP---PV----- 159
DB 698 EFKCSSENSEGCGLDGYCPSPCTCTGTIVACSRNQLKEIPRGIPAEYSLEYSENIEQI 757
QY 160 -----IRGLRGLTRLRAGNTRIAQLRPEDIAGLAALQELDVS-----NL 199
DB 758 HYERIRHLRSUTRLDLS-NNQITLSNYTANLTKLSTLLISYNKQLQCLQRHALSGLNLL 816
QY 200 SLQALPDGLSGLFPR-----LRLAARNPNFCVPLSWGPPVRESHVTLASPEET 251
DB 817 RVVSLHGNRISMLPEGSFEDLKSITHALGNSPLYDCGLKWFSDMIKLDV---BPGIA 873
QY 252 RCHFPKPKAGRLLELDYADFGCPATTTATVTRPVREPTALSSSLAPTWLSTAPA 311
DB 874 RCAEPQMKDKLILSTPSSPFCVCRGVRNRDILAKCNACFPQPCONQAQCV-----ALPQ 927

QY 312 TEAPSPSTAPPTVGVPPQ-----QDCPPSTCLNGTCHLGRHHLACLCPG 360
DB 928 REYQC-----LCOPGYHGRKCEPMIDACYGNCRNATCTVBEGRFSCQAPG 976
QY 361 FTGLYCESOM 370
DB 977 YTGARCTNI 986

RESULT 10

A36665
slit protein 1 precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 30-Apr-1991 #sequence revision 30-Apr-1991 #text_change 02-Aug-2002
A;Accession: A36665; A31640; S13523
R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A;Title: slit: an extracellular protein necessary for development of midline glia and con
A;Reference number: A36665; MUID:91099665; PMID:2176636
A;Accession: A36665
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1480 <ROT>
A;Cross-references: UNIPARC:UPI0000150PD1; GB:X53959; NID:98614; PIDN:CAA37910.1; PID:986
R;Rothberg, J.M.; Hartley, D.A.; Waicher, Z.; Artavanis-Tsakonas, S.
Cell 55, 1047-1059, 1988
A;Title: slit: An EGF-homologous locus of D. melanogaster involved in the development of
A;Reference number: A31640; MUID:89077533; PMID:3144436
A;Accession: A31640
A;Molecule type: DNA
A;Residues: 881-1188, 'G', 1185-1404, 'GT', 1463-1464, 'YHA', <RO2>
C;Cross-references: UNIPARC:UPI000016BD7A; GB:M233543; NID:9340939; PID:G514357
C;Genetics:
A;Gene: FlyBase:sl
A;Cross-references: FlyBase:FBgn0003425
A;Introns: 1351/3
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r
F;66-91/Domain: proteoglycan amino-terminal homology <PAH1>
F;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>
F;288-313/Domain: proteoglycan amino-terminal homology <PAH2>
F;323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
F;450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>
F;512-537/Domain: proteoglycan amino-terminal homology <PAH3>
F;547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
F;572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
F;596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
F;620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
F;651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>
F;708-733/Domain: proteoglycan amino-terminal homology <PAH4>
F;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
F;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
F;815-838/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR17>
F;846-890/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR18>
F;1028-1061/Domain: EGF homology <EGF>
F;1068-1099/Domain: EGF homology <EGF2>
F;1115-1148/Domain: EGF homology <EGF1>

Query Match 8.1%; Score 255.5; DB 2; Length 1480;
Best Local Similarity 21.4%; Pred. No. 4e-07;
Matches 105; Conservative 52; Mismatches 168; Indels 165; Gaps 14;

Qy	24	CPSCQCSQPOQTVECTARQGTTPRDPV-----	-----PDTVCLY	58
Db	519	CPAMCHC-EGTVDCTGRRLKEIPRDIPLHTTELLNDNDELGRISSDGLGRLPHLVKLE		577
Qy	59	VFENGITMLDASSPAGLGLQLLDLSONOIAS-----	-----LRLPRLLLDLSHNSLLALEPG	112
Db	578	LKRNQLTGIEPNAFEGASHIQELQGENKIKIENKMFGLHQLKTLNLYNQISCVMPG		637
Qy	113	ILDTAN-----	-----VEALRLAGLGLQQLDEGLFSRLRLHLDLV---	148
Db	638	SPEHLNSITSNLASNPNCNCHLAWFAECYRKKSLSNGAARCAGAPSKVRDVOIKDLPHS		697
Qy	149	-----	-----SDNQLRVP---PV-----	159
Db	698	EFKCSSENSEGLGDGYCPPSCTCTGTVVACSRNQLKEIPRGIPAEETSELYLESNEI		757
Qy	160	-----IRGLRGITRLRLAGNTFIAQLRPEDLAGLAAQLQELDVS-----	-----NL	199
Db	758	HYERIRHLRSRLRLDLS-NNQITILSNYTFANLTKLSLIISYNKLOCLORHALSGLN		816
Qy	200	SLQALPGDLSGLFPR-----	-----LRLAAARNPNCVCPLSWFGPWWVRESHVTLASPEET	251
Db	817	RVVSLHGNRISMLPEGSEFEDLKSITHALGNSPLYCDGLKWFSDWIKLDVY---	-----EPGIA	873
Qy	252	RCHPPKNAGRLLELYADFGCPATTTTATVTPTRPVVREPTALSSSLATWLSPTAPA		311
Db	874	RCAPPEQMKDKILSTPSSSFVCRGVRNDILAKNACFEQPCQNAQC-----	-----ALPQ	927
Qy	312	TEAPSPSTAPPTVGPVQP-----	-----QDCPPSTCLNGTCHLGRHHLACLCEG	360
Db	928	REYQC-----	-----LCQPGYHGKHCFMIDACYGNPCRNATCTVLEEGRFSCQCAPG	976
Qy	361	FTGLGCBESQM	370	
Db	977	YTGARCEINI	986	

RESULT 11

JC7973

synleurin - human

C;Species: Homo sapiens (man)

C;Date: 25-Aug-2003 #sequence_revision 25-Aug-2003 #text_change 15-Sep-2003

C;Accession: JC7973

R;Wang, W.; Yang, Y.; Li, L.; Shi, Y.

Biochem. Biophys. Res. Commun. 305, 981-988, 2003

A;Title: Synleurin, a novel leucine-rich repeat protein that increases the intensity of e intensity of pleiotropic cytokine responses as an adhesion protein or a receptor.

A;Reference number: JC7973; PMID:12767927

A;Accession: JC7973

A;Molecule type: mRNA

A;Residues: 1-622 <MAN>

A;Cross-references: GB:AY280614

C;Comment: This protein that is a single span transmembrane leucine-rich repeat protein e intensity of pleiotropic cytokine responses as an adhesion protein or a receptor.

C;Genetics:

A;Gene: slrn

A;Map position: Sq12.1

C;Keywords: cytokine; leucine-rich repeat; synleurin; transmembrane protein

Query Match 8.0%; Score 251; DB 2; Length 622;

Best Local Similarity 23.1%; Pred. No. 2.7e-07;

Matches 107; Conservative 52; Mismatches 142; Indels 162; Gaps 13;

Qy	2	CSRPVPLLLPLLLALGPGVQCGSCQCSQPTVFCTARQGTTPRDPVDPDTVGLVYFE	61	
Db	10	CLRLFLVVTVCYLLLLHKEILGCSVCOLCTGRQINCRNLGLSSIPKPNFPESTVFLYLTG	69	
Qy	62	NGITMLDASSPAGLPGQLLDLSONQI-----	-----ASLRLPRLLLDLSHNSLLALEPG---	112
Db	70	NNISVINESELTGLHSLVALYLDNSNILYVYPKAFVQLRHLYFLFLNNNFIKRLDPGLFK	129	
Qy	113	-----	-----ILDTAN	118
Db	130	GLLNLRLNLYOYNQVSVFPRGVFNLDLSVOYVNLORNRLTVLGSCTFFGWMALRLDLSN	189	

Qy	119	VEALRLAGLGLQLD-----EGLFSLRNLHLDVSDNQLERVPP-VIR	161
Dd	190	NNILRISESFOHLENIACLYLGSNNLTVPKSNAFEVLKSURRLSLSHNPTEAIQPFAFK	249
Qy	162	GLRGLTRLRLAGNTRIAQLRAPEDLAGAALQELDVSNLSLQALPGD-----	207
Dd	250	GLANLEYL-LLKNSRIRNVTRDGSGINNLLKHLLSHNDLEINLSDPFSLLKNLIYLYKLD	308
Qy	208	-----LSGLFFPR-----LRLAAARNPFNCVCPLS	232
Dd	309	RNRITISDNTDFENMGASLKILNLSFNFLTALHPRLVKLPSSLIIHQANSNPEWECNKLL	368
Qy	233	WFQGPWRESHVTLASPEETRECHPPKAGRLILLELDYADFGCPATTITTATPTTTPRVVRE	292
Dd	369	GLRDWLASSAITL-----NIYQMPSPSVRGALRYINITN-----CVTSINVSWAVVVRKS	420
Qy	293	P-----TAL-----SSSLAPT-----W-LSPTAPA	311
Dd	421	PHIHHKTATAMMAWHKVTTNGSPLENTETENITETWERIPTSPA	463

QY 199 LSLQALPG-----DLGLFRLRLAARPNFVCVCLSWFGPWRES 241
DB 235 NSLASVEGLASLQPNWMDRGDFISG-----NPWICDQNLSDLYRWLOAQ 282
QY 242 HVTLASPEETRCHFFPKNAGRLL 265
DB 283 KDKMSQNDTRCAGPEAVKGQILL 306

RESULT 13
A60164
platelet membrane glycoprotein V precursor - human
C:Species: Homo sapiens (man)
C>Date: 12-Jan-1993 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C:Accession: A48030; A60164; A35483; B35483; C35483; A47507; S34329
R:Iianza, F.; Morales, M.; de la Salle, C.; Cazenave, J.P.; Clemetson, K.J.; Shimomura, T.
J. Biol. Chem. 268, 20801-20807, 1993
A:Title: Cloning and characterization of the gene encoding the human platelet glycoprotein V.
A:Reference number: A48030; MUID:94012616; PMID:8407908
A:Accession: A48030
A:Molecule type: DNA
A:Residues: 1-560 <LA2>
A:Cross-references: UNIPROT:P40197; UNIPARC:UPI000004B117; EMBL:Z23091; NID:G312501; PID:R.Shimomura, T.; Fujimura, K.; Maehama, S.; Takemoto, M.; Oda, K.; Fujimoto, T.; Oyama, Blood 75, 2349-2356, 1990
A:Title: Rapid purification and characterization of human platelet glycoprotein V: the a
A:Reference number: A60164; MUID:90275263; PMID:2350580
A:Accession: A60164
A:Molecule type: protein
A:Residues: 365-384, 'X', 386-390, 'X', 392-395, 'X', 397-188-208, 'I', 210-27-50, 'X', 52-53-174-
, 'XX', 108, 'I', 61-72, 'TK', 75-77, 'V', 56-57, 'G', 479-487, 'X', 489-498, 'X', 500, 'X', 502-503, 'X',
2FD; UNIPARC:UPI000017C2F6; UNIPARC:UPI000017C2F7; UNIPARC:UPI000017C2F8;
R:Roth, G.J.; Church, T.A.; McMullen, B.A.; Williams, S.A.
Biochem. Biophys. Res. Commun. 170, 153-161, 1990
A:Title: Human platelet glycoprotein V: a surface leucine-rich glycoprotein related to a
A:Reference number: A35483; MUID:90321220; PMID:2372284
A:Accession: A35483
A:Molecule type: protein
A:Residues: 145-166, 'I', 168-169, 'X', 171-172 <RO2>
A:Cross-references: UNIPARC:UPI000017C303
A:Note: this proteolytic fragment was designated peptide M392
A:Accession: B35483
A:Molecule type: protein
A:Residues: 121-129, 'W', 131-135, 466-468, 'X', 470 <RO2>
A:Cross-references: UNIPARC:UPI000017C304; UNIPARC:UPI000017C305
A:Note: this material was designated peptide M393 but may contain two peptides
A:Accession: C35483
A:Molecule type: protein
A:Residues: 252-266, 'H', 268-272, 'X', 274-279, 'I', 281-284, 'I', 286 <RO3>
A:Cross-references: UNIPARC:UPI000017C306
A:Note: this proteolytic fragment was designated peptide M401
R:Zafar, R.S.; Walz, D.A.
Thromb. Res. 53, 31-44, 1989
A:Title: Platelet membrane glycoprotein V: characterization of the thrombin-sensitive gl
A:Reference number: A60432; MUID:89162331; PMID:2922700
A:Accession: A60432
A:Molecule type: protein
A:Residues: 477-478, 'FX', 481-485, 'E', 487, 'V', 489-492, 'NQ', 495, 'E', 497-498 <ZAF>
A:Cross-references: UNIPARC:UPI000017C307
R:Hickey, M.J.; Hagen, F.S.; Yagi, M.; Roth, G.J.
Proc. Natl. Acad. Sci. U.S.A. 90, 8327-8331, 1993
A:Title: Human platelet glycoprotein V: characterization of the polypeptide and the rela
A:Reference number: A47507; MUID:93391348; PMID:7690959
A:Accession: A47507
A>Status: preliminary; translated from GB/EMBL/DBDJB
A:Molecule type: mRNA
A:Residues: 1-560 <RES>
A:Cross-references: UNIPARC:UPI000004B117; GB:I11238; NID:G388759; PID:AAA03069.1; PID:
C:Comment: This platelet membrane protein is a substrate for thrombin.
C:Comment: The amino end of the intact protein is blocked.
C:Comment: This protein is absent in Bernard-Soulier syndrome.
C:Genetics:

A:Gene: GDB:GPS
A:Cross-references: GDB:230236; OMIM:173511
A:Map position: 5pter-5qter
C:Keywords: blocked amino end; glycoprotein; platelet; tandem repeat; transmembrane prote

Query Match 7.7%; Score 240; DB 2; Length 560;
Best Local Similarity 27.2%; Pred. No. 1e-06;
Matches 109; Conservative 28; Mismatches 111; Indels 152; Gaps 14;

QY 57 LYVFENGITMDASSFAGLPGQLLDLSONQI-----ASL--RLPRLLLDLSDHNSLLALE 110
DB 127 LFLDHNLARGIDQNNFQKLVNLQELALNQNDLFLPASLFTNLLENLKLDDLSDGNLTHLP 186
QY 111 PGILDT-ANVEALRALAGLGLQQLDEGL-----PSRLNLDH 145
DB 187 KGLGAQAQAKLERLLHNSRLVSLDGLSLNSGALTELOPHRNHRSIAPGAFDRUPNLS 246
QY 146 LDVS-----DNQLRVPVPVIRG----- 162
DB 247 LTLNRHLAFLPSALFLSHNLTLLTFENPLAEPLPGVLFGEMGGLQELWLNRTQLRTLP 306
QY 163 ---LRGLTRLRAGNT---RIAQLRPEDLAGLAALQELDV----- 196
DB 307 AAAPFNLSRLYGLVTLSPRLSALPQGAFOGLGELQVLALHNSGLTALPDGLLRGLGKLR 366
QY 197 -----SNLS-----LQALPDLSGLFPRLLRLAARPNFNCV 228
DB 367 QVSLRRNLRALPRALFRNLSLESVQLDHNQLETLPQGVFGLPRLTEVLIGHNSWRCD 426
QY 229 CPLSWFGWVRESHYTLASPER-TRCHPPKNAGRLLELDYADFGCPATTTTATVPTTR 287
DB 427 CGLGFLQWLRQ-HUGLVGGEPFPCAGFGAHGLPLNALPGDABCEPG-----PRGP 478
QY 288 PVVREPTLSSSLAPTLSPATAPATEAPSPSPSTAPPTVGP 327
DB 479 P--PRPADSSS-----EAPVHPALAPNSSEP 503

RESULT 14
JC7763
neuronal leucine-rich repeat protein-3 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: JC7763
R:Fukamachi, K.; Matsuo, Y.; Kitano, C.; Kuchino, Y.; Tsuda, H.
Biochem. Biophys. Res. Commun. 287, 257-263, 2001
A:Title: Rat neuronal leucine-rich repeat protein-3: Cloning and regulation of the gene
A:Reference number: JC7763; PMID:11549284
A:Contents: Fibrosarcoma cells
A:Accession: JC7763
A:Molecule type: mRNA
A:Residues: 1-707 <FUK>
A:Cross-references: UNIPROT:Q9ESY6; UNIPARC:UPI000004F0E2; GB:AF291437
C:Comment: This protein, a new member of the neuronal leucine-rich repeat protein family,
in protein-protein interaction and functions as a cell adhesion molecule or soluble ligar
C:Genetics:
A:Gene: nlrr-3
C:Keywords: cell adhesion

Query Match 7.6%; Score 237; DB 2; Length 707;
Best Local Similarity 20.7%; Pred. No. 2e-06;
Matches 127; Conservative 80; Mismatches 222; Indels 186; Gaps 22;

QY 6 PULLPLLLALLALGPGVQG-----CPSGCQCS-----OPQTVFCTARQGTTPV 47
DB 5 PLQIHVLGLALTAIVQAGDKKVCPLCTCIRPWFPRSIYMEASTVDCNDLGLLNFP 64
QY 48 RDVPDPTVGLYFENGITMDASSFAGLP-GLQLDLSQNIASL----- 91
DB 65 ARLPADTQILLQTNRIARIEHST--DFEVLNLTGLDLSQNLSSVTNINVQMSQLLSVY 122
QY 92 -----RLPRLILLDLDS-----HNSLLALEFGIL----- 114

Db	123	LEENKLTPEKCLYGLSNLQELIYVNHNLISAI	SPGAFVGLHNLHLRLHLNSRLQWINSK	182
QY	115	---DTANVEALRL---	AGLGLOQLDEGLFSRLRNLDLD	147
Db	183	WFALPNLEILMLGDNPIRLIKDMNFQPLKLSLVI	AGINLTVDPDDALVGLNLESI	242
QY	148	VSDNQLERVP---	PVIRGLRG---	165
Db	243	FYDNRNLKVPQVALQKAVNLKFLDLNKNPINRIR	RGDFSNMLHLKELGINNMPELVSDS	302
QY	166	-----LTRLRAGNTRIAQLRPEDLAGLAALQEL	VDNSLQAL-PGDLISGLPPRLR	216
Db	303	LAVDNLPDLRKIEATNPNRLSYIHPNAFFRLPK	LESIMLSNALSALYHGHTIESL-PNLK	361
QY	217	LIAAARNPNCVCPLSFGFWPWRSHVTLASPE	TRCHPPKKNAGRLLELDVADFGCPA	276
Db	362	EISIHNPTRCDVCIRWIN--MKNTRIRFMEPOS	LCFVDPPEFQGGQVVRQVHPRDM----	415
QY	277	TTTTATVPTTRPVVREPTALSSSL---	APTWSPTAPATEAPSPSTAPPTVGPVPQPD	333
Db	416	-----MEICLPLI-APESFPSILDVEADSVSL	CHCRATAEPQ-----PEIYWITPSGKR	463
QY	334	CPSTCLNGGTCHL-GTRHHLACLCEGFTGLY---	CESQMGQGTSPSPPTVTPRPPR--	387
Db	464	LENTLREKFYVHSEGTDIRGITPKEG--GLYTC	IATNLVGADLKSIMIKVGGFVPQDN	521
QY	388	--SLTIGIEPVSPTSRLVGLQRYLGSSVOLRS	LRLTYYNLSGPDKRLVTLRLPASLAEY	445
Db	522	NGSLNIRDIRANSVLVS---WKANSKILKSSV	KWMTAFVKTEDSQAASARIPSDVKY	578
QY	446	TVTLQRPNATYSVCV	460	
Db	579	NLTHLKPSTYKICI	593	
RESULT 15				
T42626				
secreted leucine-rich repeat-containing protein SLIT2 - mouse (fragment)				
N/Alternate names: neurogenic extracellular slit protein				
C/Species: Mus musculus (house mouse)				
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004				
C/Accession: T42626				
R/Holmes, G.P.; Negus, K.; Buttridge, L.; Raman, S.; Algar, E.; Yamada, T.; Little, M.H.				
Mech. Dev. 79, 57-72, 1998				
A/Title: Distinct but overlapping expression patterns of two vertebrate slit homologs in				
A/Reference number: 222177; PMID:99279238; PMID:10349621				
A/Accession: T42626				
A/Status: preliminary; translated from GB/EMBL/DDBJ				
A/Molecule type: mRNA				
A/Residues: 1-1025 <HOL>				
A/Cross-references: UNIPROT:Q9R1B9; UNIPARC:UPI000008B104; EMBL:AF074960; NID:g4151258;				
C/Genetics:				
A/Gene: Slit2				
C/Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein				
Query Match				
Best Local Similarity 7.4%; Score 231; DB 2: Length 1025;				
Matches 89; Conservative 32; Mismatches 122; Indels 128; Gaps 13;				
QY	24	CPSGCQCSQPQTVFCTARQGTTPRDVPPDPTVGLVYFENGITWLDASSFAGLPGLQLDL	83	
Db	223	CPSECTCLD-TXVRCNKGKLVLPKGPDKDVTLEYLDGNQFTLV-PKELSNYKHKLTLIDL	280	
QY	84	SNQIASL-----RLPRLLLDLSHNSLLALEPGILDRTANVEALRAGLGLQQLDEGLF	137	
Db	281	SNNRISTLSNQFSNMSTQLLTILSYNRLRCIPPTFD-----GLKSL-----	323	
QY	138	SLRLNLDLDVSDNQLERVPVIRGLRLTLRLAGNTRIAQLRPEDLAGLAALQELDVS	197	
Db	324	-RLSLHNDIS-----VVP-----	337	
QY	198	NLSQALPGDLGLFPRRLRLAAARNPNCVPLSWFGPWPVRSHVTLASPEETRCHPPP	257	

Db	338	-----EGAFNDLSA-----	LSHLAIGANPLYCDCNMQWLSDWKSEY----	KEPGIARCAGPG	386
Qy	258	KNAGRLLLELDVADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWSPTAPATEAPSP	317		
Db	387	EMADKLLLTTPSKKFTCQ-----	GPMDITIQAACNPCLSN	421	
Qy	318	PSTAPPTVGPVP-----	QPQDCP-----	PSTCLNGGTCHL--GTRHHLACL	356
Db	422	PCKNDGTCNNDPVDFYRCCTCPYFGKQDCDVP	FIHACISNPCKHGGTCHLKEGENAGFWCT	481	
Qy	357	CPEGFTGLYCE	367		
Db	482	CADGEGENCE	492		

Search completed: January 28, 2007, 17:28:03
Job time : 71 secs